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(54) Title: RECOMBINANT IL-18 ANTAGONISTS USEFUL IN TREATMENT OF IL-18 MEDIATED DISORDERS

### (57) Abstract

Chimeric, humanized and other IL-18 mAbs, derived from high affinity neutralizing mAbs, pharmaceutical compositions containing same, methods of treatment and diagnostics are provided.

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RECOMBINANT IL-18 ANTAGONISTS USEFUL IN TREATMENT OF IL-18  
MEDIATED DISORDERS

5    FIELD OF THE INVENTION

The present invention relates generally to the field of antibodies and altered antibodies, useful in the treatment and diagnosis of conditions mediated by IL-18, and more specifically to mAbs, Fabs, chimeric and humanized antibodies.

10    BACKGROUND OF THE INVENTION

Human interleukin-18 is a recently identified cytokine that is synthesized as a biologically inactive 193 amino acid precursor protein (Ushio et al., *J. Immunol.* 156:4274, 1996). Cleavage of the precursor protein, for example by caspase-1 or caspase-4, liberates the 156 amino acid mature protein (Gu et al., *Science* 275:206, 15 1997; Ghayur et al., *Nature* 386:619, 1997), which exhibits biological activities that include the costimulation of T cell proliferation, the enhancement of NK cell cytotoxicity, the induction of IFN- $\gamma$  production by T cells and NK cells, and the potentiation of T helper type 1 (Th1) differentiation (Okamura et al., *Nature* 378:88, 1995; Ushio et al., *J. Immunol.* 156:4274, 1996; Micallef et al., *Eur. J. Immunol.* 20 26:1647, 1996; Kohno et al., *J. Immunol.* 158:1541, 1997; Zhang et al., *Infect. Immunol.* 65:3594, 1997; Robinson et al., *Immunity* 7:571, 1997). In addition, IL-18 is an efficacious inducer of human monocyte proinflammatory mediators, including IL-8, tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), and prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) (Ushio, S. et al., *J. Immunol.* 156:4274-4279, 1996; Puren, A.J. et al., *J. Clin. Invest.* 25 10:711-721, 1997; Podolin et al., *J. Immunol.* submitted, 1999).

The previously cloned IL-1 receptor-related protein (IL-1Rrp) (Parnet et al., *J. Biol. Chem.* 271:3967, 1996) was recently identified as a subunit of the IL-18 receptor ( $K_d = 18$  nM) (Torigoe et al., *J. Biol. Chem.* 272:25737, 1997). A second subunit of the IL-18 receptor exhibits homology to the IL-1 receptor accessory protein, and has been termed AcPL (for accessory protein-like). Expression of both IL-1Rrp and AcPL are required for IL-18-induced NF- $\kappa$ B and JNK activation (Born et al., *J. Biol. Chem.* 273:29445, 1998). In addition to NF- $\kappa$ B and JNK, IL-18 signals through IL-1 receptor-associated kinase (IRAK), p56lck (LCK), and mitogen-activated protein kinase (MAPK) (Micallef et al., *Eur. J. Immunol.* 30 26:1647, 1996; Matsumoto et al., *Biophys Biochem. Res. Comm.* 234:454, 1997; Tsuji-Takayama et al., *Biochem. Biophys. Res. Comm.* 237:126, 1997).

Th1 cells, which produce proinflammatory cytokines such as IFN- $\gamma$ , IL-2 and TNF- $\beta$  (Mosmann et al., J. Immunol. 136:2348, 1986), have been implicated in mediating many of autoimmune diseases, including multiple sclerosis (MS), rheumatoid arthritis (RA), type 1, or insulin dependent, diabetes (IDDM). 5 inflammatory bowel disease (IBD), and psoriasis (Mosmann and Sad, Immunol. Today 17:138, 1996). Thus, antagonism of a Th1-promoting cytokine such as IL-18 would be expected to inhibit disease development. IL-18 specific mAbs could be used as an antagonist.

The role of IL-18 in the development of autoimmune diseases has been 10 demonstrated. Accordingly, it has been demonstrated that IL-18 expression is significantly increased in the pancreas and spleen of the nonobese diabetic (NOD) mouse immediately prior to the onset of disease (Rothe et al., J. Clin. Invest. 99:469, 1997). Similarly, IL-18 levels have been shown to be markedly elevated in the synovial fluid of rheumatoid arthritis patients (Kawashima et al., Arthritis and 15 Rheumatism 39:598, 1996). Furthermore, it has been demonstrated that IL-18 administration increases the clinical severity of murine experimental allergic encephalomyelitis (EAE), a Th1-mediated autoimmune disease that is a model for multiple sclerosis. In addition, it has been shown that neutralizing anti-rat IL-18 antiserum prevents the development of EAE in female Lewis rats (Wildbaum et al., J. Immunol. 161:6368, 1998). Accordingly, IL-18 is a desirable target for the 20 development of a novel therapeutic for autoimmunity.

Taniguchi et al., J. Immunol. Methods 206:107, describe seven murine and six rat anti-human IL-18 mAbs, which bind to four distinct antigenic sites. One of the murine mAbs (#125-2H), and the six rat mAbs inhibit IL-18-induced IFN- $\gamma$  25 production by KG-1 cells, with the rat mAbs exhibiting neutralizing activities 10-fold lower than that of #125-2H. As demonstrated by Western blot analysis, three of the murine mAbs, but none of the rat mAbs, are strongly reactive with membrane-bound human IL-18. In addition, an enzyme-linked immunosorbent assay (ELISA) to detect human IL-18 is described, utilizing #125-2H and a rat mAb. The limit of 30 detection of this ELISA is 10 pg/ml.

European patent application EP 0 712 931 discloses two mouse anti-human IL-18 mAbs, H1 (IgG1) and H2 (IgM). As demonstrated by Western blot analysis, both mAbs react with membrane-bound human IL-18, but not with membrane-bound human IL-12. H1 is utilized in an immunoaffinity chromatography protocol 35 to purify human IL-18, and in an ELISA to measure human IL-18. H2 is utilized in a radioimmunoassay to measure human IL-18.

Neutralizing IL-18 antibodies may potentially be useful in relieving autoimmune diseases and related symptoms in man. Hence there is a need in the art for a high affinity IL-18 antagonist, such as a neutralizing monoclonal antibody to human interleukin 18, which would reduce Th1 differentiation and proliferation and thus autoimmune diseases and related symptoms.

### SUMMARY OF THE INVENTION

In a first aspect, the present invention provides rodent (e.g., rat and murine) neutralizing monoclonal antibodies specific for human interleukin-18 and having a binding affinity characterized by a dissociation constant equal to or less than about  $3.9 \times 10^{-11}$  M as described in the detailed description. Exemplary of such monoclonal antibodies are the rat monoclonal antibody 2C10 and rat and murine monoclonal antibodies such as 14B7 and 13G9. Another aspect of the invention are hybridomas such as 19522C10(2)F2(1)A1, 195214B7(1)H10 and 187413G9(3)F12.

In a related aspect, the present invention provides neutralizing Fab fragments or  $F(ab')_2$  fragments thereof specific for human interleukin-18 produced by deleting the Fc region of the rodent neutralizing monoclonal antibodies of the present invention.

In still another related aspect, the present invention provides an altered antibody specific for human interleukin-18 which comprises complementarity determining regions (CDRs) derived from a non-human neutralizing monoclonal antibody (mAb) characterized by a dissociation constant equal to or less than about  $3.9 \times 10^{-11}$  M for human interleukin-18 and nucleic acid molecules encoding the same. When the altered antibody is a humanized antibody, the sequences that encode complementarity determining regions (CDRs) from a non-human immunoglobulin are inserted into a first immunoglobulin partner in which at least one, and preferably all complementarity determining regions (CDRs) of the first immunoglobulin partner are replaced by CDRs from the non-human monoclonal antibody. Preferably, the first immunoglobulin partner is operatively linked to a second immunoglobulin partner as well, which comprises all or a part of an immunoglobulin constant chain.

In a related aspect, the present invention provides CDRs derived from non-human neutralizing monoclonal antibodies (mAbs) characterized by a dissociation constant equal to or less than about  $3.9 \times 10^{-11}$  M for human interleukin-18, and nucleic acid molecules encoding such CDRs.

In still another aspect, there is provided a chimeric antibody containing human heavy and light chain constant regions and heavy and light chain variable

regions derived from non-human neutralizing monoclonal antibodies characterized by a dissociation constant equal to or less than about  $3.9 \times 10^{-11}$  M for human interleukin-18.

5 In yet another aspect, the present invention provides a pharmaceutical composition which contains one (or more) of the above described altered antibodies and a pharmaceutically acceptable carrier.

10 In a further aspect, the present invention provides a method for treating conditions in humans associated with excess Th1 production, for example autoimmune diseases, by administering to said human an effective amount of the pharmaceutical composition of the invention.

In yet another aspect, the present invention provides methods for, and components useful in, the recombinant production of altered antibodies (e.g., engineered antibodies, CDRs, Fab or F(ab)<sub>2</sub> fragments, or analogs thereof) which are derived from non-human neutralizing monoclonal antibodies (mAbs) characterized 15 by a dissociation constant equal to or less than  $3.9 \times 10^{-11}$  M for human IL-18. These components include isolated nucleic acid sequences encoding same, recombinant plasmids containing the nucleic acid sequences under the control of selected regulatory sequences which are capable of directing the expression thereof in host cells (preferably mammalian) transfected with the recombinant plasmids. 20 The production method involves culturing a transfected host cell line of the present invention under conditions such that an altered antibody, preferably a humanized antibody, is expressed in said cells and isolating the expressed product therefrom.

25 In yet another aspect of the invention is a method to diagnose conditions associated with excess Th1 production in a human which comprises obtaining a sample of biological fluid from a patient and allowing the antibodies and altered antibodies of the instant invention to come in contact with such sample under conditions such that an IL-18/antibody (monoclonal or altered) complex is formed and detecting the presence or absence of said IL-18/antibody complex.

30 Other aspects and advantages of the present invention are described further in the detailed description and the preferred embodiments thereof.

#### BRIEF DESCRIPTION OF THE DRAWINGS

35 Fig. 1 [SEQ ID NOS: 1 and 2] illustrates the light chain variable region for the rat antibody 2C10. Fig. 1 includes sequence data for both strands. The boxed areas indicate the CDR's [SEQ ID NOS: 3-8]. The bolded area indicates the degenerate primer sequence.

Fig. 2. [SEQ ID NOS: 9 and 10] illustrates the heavy chain variable region for the rat antibody 2C10. Fig. 2 includes sequence data for both strands. The boxed areas indicate the CDR's [SEQ ID NOS: 11-16]. The bolded area indicates the degenerate primer sequence.

5 Fig. 3 [SEQ ID NOS: 17 and 18] illustrates the light chain variable region for the murine antibody 13G9. Fig. 3 includes sequence data for both strands. The boxed areas indicate the CDR's [SEQ ID NOS: 19-24]. The bolded area indicates the degenerate primer sequence.

10 Fig 4 [SEQ ID NOS: 25 and 26] illustrates the heavy chain variable region for the murine antibody 13G9. Fig. 4 includes sequence data for both strands. The boxed areas indicate the CDR's [SEQ ID NOS: 27-32]. The bolded area indicates the degenerate primer sequence.

15 Fig 5 [SEQ ID NOS: 33 and 34] illustrates the light chain variable region for the rat antibody 14B7. Fig. 5 includes sequence data for both strands. The boxed areas indicate the CDR's [SEQ ID NOS: 35-40]. The bolded area indicates the degenerate primer sequence.

20 Fig 6 [SEQ ID NOS: 41 and 42] illustrates the heavy chain variable region for the rat antibody 14B7. Fig. 6 includes sequence data for both strands. The boxed areas indicate the CDR's [SEQ ID NOS: 43-48]. The bolded area indicates the degenerate primer sequence.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a variety of antibodies, altered antibodies and fragments thereof, which are characterized by human IL-18 binding specificity, neutralizing activity, and high affinity for human IL-18 as exemplified in rat monoclonal antibody 2C10, murine monoclonal antibody 13G9 and rat monoclonal antibody 14B7. The antibodies of the present invention were prepared by conventional hybridoma techniques to generate novel neutralizing antibodies. These products are useful in therapeutic and pharmaceutical compositions for treating IL-18-mediated disorders, e.g. autoimmune diseases, including multiple sclerosis (MS), rheumatoid arthritis (RA), type 1, or insulin dependent, diabetes (IDDM), inflammatory bowel disease (IBD), and psoriasis (Mosmann and Sad, Immunol. Today 17:138, 1996). These products are also useful in the diagnosis of IL-18-mediated conditions by measurement (e.g., enzyme linked immunosorbent assay (ELISA)) of endogenous IL-18 levels in humans or IL-18 released *ex vivo* from activated cells.

*I. Definitions.*

"Altered antibody" refers to a protein encoded by an altered immunoglobulin coding region, which may be obtained by expression in a selected host cell. Such altered antibodies are engineered antibodies (e.g., chimeric or humanized antibodies) or antibody fragments lacking all or part of an immunoglobulin constant region, e.g., Fv, Fab, or F(ab)<sub>2</sub> and the like.

"Altered immunoglobulin coding region" refers to a nucleic acid sequence encoding altered antibody of the invention. When the altered antibody is a CDR-grafted or humanized antibody, the sequences that encode the complementarity determining regions (CDRs) from a non-human immunoglobulin are inserted into a first immunoglobulin partner comprising human variable framework sequences. Optionally, the first immunoglobulin partner is operatively linked to a second immunoglobulin partner.

"First immunoglobulin partner" refers to a nucleic acid sequence encoding a human framework or human immunoglobulin variable region in which the native (or naturally-occurring) CDR-encoding regions are replaced by the CDR-encoding regions of a donor antibody. The human variable region can be an immunoglobulin heavy chain, a light chain (or both chains), an analog or functional fragments thereof. Such CDR regions, located within the variable region of antibodies (immunoglobulins) can be determined by known methods in the art. For example Kabat et al. (Sequences of Proteins of Immunological Interest, 4th Ed., U.S. Department of Health and Human Services, National Institutes of Health (1987)) disclose rules for locating CDRs. In addition, computer programs are known which are useful for identifying CDR regions/structures.

"Neutralizing" refers to an antibody that inhibits IL-18 activity by preventing the binding of human IL-18 to its specific receptor or by inhibiting the signaling of IL-18 through its receptor, should binding occur. A mAb is neutralizing if it is 90% effective, preferably 95% effective and most preferably 100% effective in inhibiting IL-18 activity as measured in the IL-18 neutralization assay, see Example 1 and Table I.

The term "high affinity" refers to an antibody having a binding affinity characterized by a K<sub>d</sub> equal to or less than 3.9 x 10<sup>-11</sup> M for human IL-18 as determined by optical biosensor analysis (see Example 2 and Table I).

By "binding specificity for human IL-18" is meant a higher affinity for human IL-18 than murine, or other IL-18.

"Second immunoglobulin partner" refers to another nucleotide sequence encoding a protein or peptide to which the first immunoglobulin partner is fused in

frame or by means of an optional conventional linker sequence (i.e., operatively linked). Preferably it is an immunoglobulin gene. The second immunoglobulin partner may include a nucleic acid sequence encoding the entire constant region for the same (i.e., homologous - the first and second altered antibodies are derived from the same source) or an additional (i.e., heterologous) antibody of interest. It may be an immunoglobulin heavy chain or light chain (or both chains as part of a single polypeptide). The second immunoglobulin partner is not limited to a particular immunoglobulin class or isotype. In addition, the second immunoglobulin partner may comprise part of an immunoglobulin constant region, such as found in a Fab, or F(ab)<sub>2</sub> (i.e., a discrete part of an appropriate human constant region or framework region). Such second immunoglobulin partner may also comprise a sequence encoding an integral membrane protein exposed on the outer surface of a host cell, e.g., as part of a phage display library, or a sequence encoding a protein for analytical or diagnostic detection, e.g., horseradish peroxidase,  $\beta$ -galactosidase, etc.

The terms Fv, Fc, Fd, Fab, or F(ab)<sub>2</sub> are used with their standard meanings (see, e.g., Harlow et al., Antibodies A Laboratory Manual, Cold Spring Harbor Laboratory, (1988)).

As used herein, an "engineered antibody" describes a type of altered antibody, i.e., a full-length synthetic antibody (e.g., a chimeric or humanized antibody as opposed to an antibody fragment) in which a portion of the light and/or heavy chain variable domains of a selected acceptor antibody are replaced by analogous parts from one or more donor antibodies which have specificity for the selected epitope. For example, such molecules may include antibodies characterized by a humanized heavy chain associated with an unmodified light chain (or chimeric light chain), or vice versa. Engineered antibodies may also be characterized by alteration of the nucleic acid sequences encoding the acceptor antibody light and/or heavy variable domain framework regions in order to retain donor antibody binding specificity. These antibodies can comprise replacement of one or more CDRs (preferably all) from the acceptor antibody with CDRs from a donor antibody described herein.

A "chimeric antibody" refers to a type of engineered antibody which contains naturally-occurring variable region (light chain and heavy chains) derived from a donor antibody in association with light and heavy chain constant regions derived from an acceptor antibody.

A "humanized antibody" refers to a type of engineered antibody having its CDRs derived from a non-human donor immunoglobulin, the remaining immunoglobulin-derived parts of the molecule being derived from one (or more)

human immunoglobulin(s). In addition, framework support residues may be altered to preserve binding affinity (see, e.g., Queen et al., Proc. Natl Acad Sci USA. 86:10029-10032 (1989). Hodgson et al., Bio/Technology, 9:421 (1991)).

The term "donor antibody" refers to an antibody (monoclonal, or recombinant) which contributes the nucleic acid sequences of its variable regions, CDRs, or other functional fragments or analogs thereof to a first immunoglobulin partner, so as to provide the altered immunoglobulin coding region and resulting expressed altered antibody with the antigenic specificity and neutralizing activity characteristic of the donor antibody. One donor antibody suitable for use in this invention is a non-human neutralizing monoclonal antibody (i.e., rat) designated as 2C10. The antibody 2C10 is defined as a high affinity, human-IL-18 specific (i.e., does not recognize murine IL-18), neutralizing antibody of isotype IgG<sub>1,K</sub> having the variable light chain DNA and amino acid sequences of SEQ ID NOs: 1 and 2 and respectively, the variable heavy chain DNA and amino acid sequences of SEQ ID NOs: 9 and 10 on a suitable murine IgG constant region.

The term "acceptor antibody" refers to an antibody (monoclonal, or recombinant) heterologous to the donor antibody, which contributes all (or any portion, but preferably all) of the nucleic acid sequences encoding its heavy and/or light chain framework regions and/or its heavy and/or light chain constant regions to the first immunoglobulin partner. Preferably a human antibody is the acceptor antibody.

"CDRs" are defined as the complementarity determining region amino acid sequences of an antibody which are the hypervariable regions of immunoglobulin heavy and light chains. See, e.g., Kabat et al., Sequences of Proteins of Immunological Interest, 4th Ed., U.S. Department of Health and Human Services, National Institutes of Health (1987). There are three heavy chain and three light chain CDRs (or CDR regions) in the variable portion of an immunoglobulin. Thus, "CDRs" as used herein refers to all three heavy chain CDRs, or all three light chain CDRs (or both all heavy and all light chain CDRs, if appropriate).

CDRs provide the majority of contact residues for the binding of the antibody to the antigen or epitope. CDRs of interest in this invention are derived from donor antibody variable heavy and light chain sequences, and include analogs of the naturally occurring CDRs, which analogs also share or retain the same antigen binding specificity and/or neutralizing ability as the donor antibody from which they were derived.

By sharing the antigen binding specificity or neutralizing ability is meant, for example, that although mAb 2C10 may be characterized by a certain level of antigen

affinity, a CDR encoded by a nucleic acid sequence of 2C10 in an appropriate structural environment may have a lower, or higher affinity. It is expected that CDRs of 2C10 in such environments will nevertheless recognize the same epitope(s) as 2C10. Exemplary light chain CDRs of 2C10 include

- 5 SEQ ID NO: 3;  
SEQ ID NO: 5;  
SEQ ID NO: 7;  
and exemplary heavy chain CDRs of 2C10 include  
SEQ ID NO: 11;  
10 SEQ ID NO: 13;  
and SEQ ID NO: 15.

A "functional fragment" is a partial heavy or light chain variable sequence (e.g., minor deletions at the amino or carboxy terminus of the immunoglobulin variable region) which retains the same antigen binding specificity and/or neutralizing ability as the antibody from which the fragment was derived.

An "analog" is an amino acid sequence modified by at least one amino acid, wherein said modification can be chemical or a substitution or a rearrangement of a few amino acids (i.e., no more than 10), which modification permits the amino acid sequence to retain the biological characteristics, e.g., antigen specificity and high affinity, of the unmodified sequence. For example, (silent) mutations can be constructed, via substitutions, when certain endonuclease restriction sites are created within or surrounding CDR-encoding regions.

Analogs may also arise as allelic variations. An "allelic variation or modification" is an alteration in the nucleic acid sequence encoding the amino acid or peptide sequences of the invention. Such variations or modifications may be due to degeneracy in the genetic code or may be deliberately engineered to provide desired characteristics. These variations or modifications may or may not result in alterations in any encoded amino acid sequence.

The term "effector agents" refers to non-protein carrier molecules to which the altered antibodies, and/or natural or synthetic light or heavy chains of the donor antibody or other fragments of the donor antibody may be associated by conventional means. Such non-protein carriers can include conventional carriers used in the diagnostic field, e.g., polystyrene or other plastic beads, polysaccharides, e.g., as used in the BIACore [Pharmacia] system, or other non-protein substances useful in the medical field and safe for administration to humans and animals. Other effector agents may include a macrocycle, for chelating a heavy metal atom, or

radioisotopes. Such effector agents may also be useful to increase the half-life of the altered antibodies, e.g., polyethylene glycol.

## *II. High Affinity IL-18 Monoclonal Antibodies*

5 For use in constructing the antibodies, altered antibodies and fragments of this invention, a non-human species (for example, bovine, ovine, monkey, chicken, rodent (e.g., murine and rat), etc.) may be employed to generate a desirable immunoglobulin upon presentation with native human IL-18 or a peptide epitope therefrom. Conventional hybridoma techniques are employed to provide a  
10 hybridoma cell line secreting a non-human mAb to IL-18. Such hybridomas are then screened for binding using IL-18 coated to 96-well plates, as described in the Examples section, or alternatively with biotinylated IL-18 bound to a streptavidin coated plate.

One exemplary, high affinity, neutralizing mAb of this instant invention is  
15 mAb 2C10, a rat antibody which can be used for the development of a chimeric or humanized antibody, described in more detail in examples below. The 2C10 mAb is characterized by an antigen binding specificity for human IL-18 of about  $K_d$   $3.9 \times 10^{-11}$  M. This mAb is characterized by being isotype IgG<sub>1,K</sub>.

Another desirable donor antibody is the murine mAb 13G9. This mAb is  
20 characterized by being isotype IgG<sub>1,K</sub>. The mAb has a dissociation constant for IL-18 of about  $12 \times 10^{-9}$  M.

Yet, another desirable donor antibody is the rat mAb, 14B7. This mAb is characterized by having a dissociation constant for IL-18 about  $1.5 \times 10^{-10}$  M. 14B7 is also characterized by being isotype IgG<sub>1,K</sub>.

25 This invention is not limited to the use of the 13G9, 2C10, 14B7, or their hypervariable (i.e., CDR) sequences. Any other appropriate high affinity IL-18 antibodies characterized by a dissociation constant equal or less than about  $3.9 \times 10^{-11}$  M for human IL-18 and corresponding anti-IL-18 CDRs may be substituted therefor. Wherever in the following description the donor antibody is identified as 13G9,  
30 2C10, 14B7, this designation is made for illustration and simplicity of description only.

### III. Antibody Fragments

The present invention also includes the use of Fab fragments or  $F(ab')_2$  fragments derived from mAbs directed against human IL-18. These fragments are useful as agents protective *in vivo* against IL-18 and Th1-mediated conditions or *in vitro* as part of an IL-18 diagnostic. A Fab fragment contains the entire light chain and amino terminal portion of the heavy chain; and an  $F(ab')_2$  fragment is the fragment formed by two Fab fragments bound by disulfide bonds. MAbs 13G9, 2C10, 14B7, and other similar high affinity, IL-18 binding antibodies, provide sources of Fab fragments and  $F(ab')_2$  fragments which can be obtained by conventional means, e.g., cleavage of the mAb with the appropriate proteolytic enzymes, papain and/or pepsin, or by recombinant methods. These Fab and  $F(ab')_2$  fragments are useful themselves as therapeutic, prophylactic or diagnostic agents, and as donors of sequences including the variable regions and CDR sequences useful in the formation of recombinant or humanized antibodies as described herein.

The Fab and  $F(ab')_2$  fragments can be constructed via a combinatorial phage library (see, e.g., Winter et al., *Ann. Rev. Immunol.*, **12**:433-455 (1994)) or via immunoglobulin chain shuffling (see, e.g., Marks et al., *Bio/Technology*, **10**:779-783 (1992), which are both hereby incorporated by reference in their entirety) wherein the Fd or  $v_H$  immunoglobulin from a selected antibody (e.g., 13G9) is allowed to associate with a repertoire of light chain immunoglobulins,  $v_L$  (or  $v_K$ ), to form novel Fabs. Conversely, the light chain immunoglobulin from a selected antibody may be allowed to associate with a repertoire of heavy chain immunoglobulins,  $v_H$  (or Fd), to form novel Fabs.

### IV. Anti-IL-18 Amino Acid and Nucleotide Sequences of Interest

The mAb 2C10 or other antibodies described above may contribute sequences, such as variable heavy and/or light chain peptide sequences, framework sequences, CDR sequences, functional fragments, and analogs thereof, and the nucleic acid sequences encoding them, useful in designing and obtaining various altered antibodies which are characterized by the antigen binding specificity of the donor antibody.

As one example, the present invention provides variable light chain and variable heavy chain sequences from the IL-18 mAb 2C10 and sequences derived therefrom.

The nucleic acid sequences of this invention, or fragments thereof, encoding the variable light chain and heavy chain peptide sequences are also useful for mutagenic introduction of specific changes within the nucleic acid sequences

encoding the CDRs or framework regions, and for incorporation of the resulting modified or fusion nucleic acid sequence into a plasmid for expression..

Taking into account the degeneracy of the genetic code, various coding sequences may be constructed which encode the variable heavy and light chain  
5 amino acid sequences, and CDR sequences of the invention as well as functional fragments and analogs thereof which share the antigen specificity of the donor antibody. The isolated nucleic acid sequences of this invention, or fragments thereof, encoding the variable chain peptide sequences or CDRs can be used to produce altered antibodies, e.g., chimeric or humanized antibodies, or other  
10 engineered antibodies of this invention when operatively combined with a second immunoglobulin partner.

It should be noted that in addition to isolated nucleic acid sequences encoding portions of the altered antibody and antibodies described herein, other such nucleic acid sequences are encompassed by the present invention, such as those  
15 complementary to the native CDR-encoding sequences or complementary to the modified human framework regions surrounding the CDR-encoding regions. Useful DNA sequences include those sequences which hybridize under stringent hybridization conditions [see, T. Maniatis et al, Molecular Cloning (A Laboratory Manual), Cold Spring Harbor Laboratory (1982), pages 387 to 389] to the DNA  
20 sequences. An example of one such stringent hybridization condition is hybridization at 4XSSC at 65°C, followed by a washing in 0.1XSSC at 65°C for an hour. Alternatively an exemplary stringent hybridization condition is in 50% formamide, 4XSSC at 42°C. Preferably, these hybridizing DNA sequences are at least about 18 nucleotides in length, i.e., about the size of a CDR.  
25

#### V. *Altered Immunoglobulin Molecules And Altered Antibodies*

Altered immunoglobulin molecules can encode altered antibodies which include engineered antibodies such as chimeric antibodies and humanized antibodies. A desired altered immunoglobulin coding region contains CDR-  
30 encoding regions that encode peptides having the antigen specificity of an IL-18 antibody, preferably a high affinity antibody such as provided by the present invention, inserted into a first immunoglobulin partner (a human framework or human immunoglobulin variable region).

Preferably, the first immunoglobulin partner is operatively linked to a second  
35 immunoglobulin partner. The second immunoglobulin partner is defined above, and may include a sequence encoding a second antibody region of interest, for example an Fc region. Second immunoglobulin partners may also include sequences

encoding another immunoglobulin to which the light or heavy chain constant region is fused in frame or by means of a linker sequence. Engineered antibodies directed against functional fragments or analogs of IL-18 may be designed to elicit enhanced binding with the same antibody.

5        The second immunoglobulin partner may also be associated with effector agents as defined above, including non-protein carrier molecules, to which the second immunoglobulin partner may be operatively linked by conventional means.

Fusion or linkage between the second immunoglobulin partners, e.g., antibody sequences, and the effector agent may be by any suitable means, e.g., by  
10      conventional covalent or ionic bonds, protein fusions, or hetero-bifunctional cross-linkers, e.g., carbodiimide, glutaraldehyde, and the like. Such techniques are known in the art and readily described in conventional chemistry and biochemistry texts.

Additionally, conventional linker sequences which simply provide for a desired amount of space between the second immunoglobulin partner and the  
15      effector agent may also be constructed into the altered immunoglobulin coding region. The design of such linkers is well known to those of skill in the art.

In addition, signal sequences for the molecules of the invention may be modified to enhance expression.

An exemplary altered antibody contains a variable heavy and/or light chain  
20      peptide or protein sequence having the antigen specificity of mAb 2C10, e.g., the V<sub>H</sub> and V<sub>L</sub> chains. Still another desirable altered antibody of this invention is characterized by the amino acid sequence containing at least one, and preferably all of the CDRs of the variable region of the heavy and/or light chains of the rat antibody molecule 2C10 with the remaining sequences being derived from a human  
25      source, or a functional fragment or analog thereof.

In still a further embodiment, the engineered antibody of the invention may have attached to it an additional agent. For example, the procedure of recombinant DNA technology may be used to produce an engineered antibody of the invention in which the Fc fragment or CH2 CH3 domain of a complete antibody molecule has  
30      been replaced by an enzyme or other detectable molecule (i.e., a polypeptide effector or reporter molecule).

The second immunoglobulin partner may also be operatively linked to a non-immunoglobulin peptide, protein or fragment thereof heterologous to the CDR-containing sequence, for example, having the antigen specificity of rat 2C10. The  
35      resulting protein may exhibit both anti-IL-18 antigen specificity and characteristics of the non-immunoglobulin upon expression. That fusion partner characteristic may be, e.g., a functional characteristic such as another binding or receptor domain, or a

therapeutic characteristic if the fusion partner is itself a therapeutic protein, or additional antigenic characteristics.

Another desirable protein of this invention may comprise a complete antibody molecule, having full length heavy and light chains, or any discrete

5 fragment thereof, such as the Fab or F(ab'), fragments, a heavy chain dimer, or any minimal recombinant fragments thereof such as an F<sub>v</sub> or a single-chain antibody (SCA) or any other molecule with the same specificity as the selected donor mAb, e.g., mAb 2C10. Such protein may be used in the form of an altered antibody, or may be used in its unfused form.

10 Whenever the second immunoglobulin partner is derived from an antibody different from the donor antibody, e.g., any isotype or class of immunoglobulin framework or constant regions, an engineered antibody results. Engineered antibodies can comprise immunoglobulin (Ig) constant regions and variable framework regions from one source, e.g., the acceptor antibody, and one or more

15 (preferably all) CDRs from the donor antibody, e.g., the anti-IL-18 antibody described herein. In addition, alterations, e.g., deletions, substitutions, or additions, of the acceptor mAb light and/or heavy variable domain framework region at the nucleic acid or amino acid levels, or the donor CDR regions may be made in order to retain donor antibody antigen binding specificity.

20 Such engineered antibodies are designed to employ one (or both) of the variable heavy and/or light chains of the IL-18 mAb (optionally modified as described) or one or more of the below-identified heavy or light chain CDRs. The engineered antibodies would be expected to be neutralizing, i.e., they desirably block binding to the receptor of the IL-18 protein and they also block or prevent  
25 proliferation of IL-18 dependent cells.

Such engineered antibodies may include a humanized antibody containing the framework regions of a selected human immunoglobulin or subtype, or a chimeric antibody containing the human heavy and light chain constant regions fused to the IL-18 antibody functional fragments. A suitable human (or other animal) acceptor antibody may be one selected from a conventional database, e.g., the KABAT® database, Los Alamos database, and Swiss Protein database, by homology to the nucleotide and amino acid sequences of the donor antibody. A human antibody characterized by a homology to the framework regions of the donor antibody (on an amino acid basis) may be suitable to provide a heavy chain constant region and/or a heavy chain variable framework region for insertion of the donor CDRs. A suitable acceptor antibody capable of donating light chain constant or variable framework regions may be selected in a similar manner. It should be noted

that the acceptor antibody heavy and light chains are not required to originate from the same acceptor antibody.

Desirably the heterologous framework and constant regions are selected from human immunoglobulin classes and isotypes, such as IgG (subtypes 1 through 4).

5 IgM, IgA, and IgE. However, the acceptor antibody need not comprise only human immunoglobulin protein sequences. For instance a gene may be constructed in which a DNA sequence encoding part of a human immunoglobulin chain is fused to a DNA sequence encoding a non-immunoglobulin amino acid sequence such as a polypeptide effector or reporter molecule.

10 One example of a particularly desirable humanized antibody would contain CDRs of 2C10 inserted onto the framework regions of a selected human antibody sequence. For neutralizing humanized antibodies, one, two or preferably three CDRs from the IL-18 antibody heavy chain and/or light chain variable regions are inserted into the framework regions of the selected human antibody sequence,

15 replacing the native CDRs of the latter antibody.

Preferably, in a humanized antibody, the variable domains in both human heavy and light chains have been engineered by one or more CDR replacements. It is possible to use all six CDRs, or various combinations of less than the six CDRs. Preferably all six CDRs are replaced. It is possible to replace the CDRs only in the  
20 human heavy chain, using as light chain the unmodified light chain from the human acceptor antibody. Still alternatively, a compatible light chain may be selected from another human antibody by recourse to the conventional antibody databases. The remainder of the engineered antibody may be derived from any suitable acceptor human immunoglobulin.

25 The engineered humanized antibody thus preferably has the structure of a natural human antibody or a fragment thereof, and possesses the combination of properties required for effective therapeutic use, e.g., treatment of IL-18 mediated inflammatory diseases in man, or for diagnostic uses.

As another example, an engineered antibody may contain CDRs of the  
30 variable light chain region of 2C10 and CDRs of the variable heavy chain region of 13G9. The resulting humanized antibody should be characterized by the same antigen binding specificity and high affinity of mAb 2C10.

It will be understood by those skilled in the art that an engineered antibody may be further modified by changes in variable domain amino acids without  
35 necessarily affecting the specificity and high affinity of the donor antibody (i.e., an analog). It is anticipated that heavy and light chain amino acids may be substituted by other amino acids either in the variable domain frameworks or CDRs or both.

In addition, the constant region may be altered to enhance or decrease selective properties of the molecules of the instant invention. For example, dimerization, binding to Fc receptors, or the ability to bind and activate complement (see, e.g., Angal et al., *Mol. Immunol.* 30:105-108 (1993), Xu et al., *J. Biol. Chem.*, 5 269:3469-3474 (1994), Winter et al., EP 307,434-B).

An altered antibody which is a chimeric antibody differs from the humanized antibodies described above by providing the entire non-human donor antibody heavy chain and light chain variable regions, including framework regions, in association with human immunoglobulin constant regions for both chains. It is anticipated that 10 chimeric antibodies which retain additional non-human sequence relative to humanized antibodies of this invention may elicit a significant immune response in humans.

Such antibodies could be useful in the prevention and treatment of IL-18 mediated disorders, as discussed below.

15

#### *VI. Production Of Altered Antibodies And Engineered Antibodies*

Preferably, the variable light and/or heavy chain sequences and the CDRs of mAb 2C10 or other suitable donor mAbs, and their encoding nucleic acid sequences, are utilized in the construction of altered antibodies, preferably humanized 20 antibodies, of this invention, by the following process. The same or similar techniques may also be employed to generate other embodiments of this invention.

A hybridoma producing a selected donor mAb, e.g., the rat antibody 2C10, is conventionally cloned, and the DNA of its heavy and light chain variable regions obtained by techniques known to one of skill in the art, e.g., the techniques described 25 in Sambrook et al., (*Molecular Cloning (A Laboratory Manual)*, 2nd edition, Cold Spring Harbor Laboratory (1989)). The variable heavy and light regions of 2C10 containing at least the CDR-encoding regions and those portions of the acceptor mAb light and/or heavy variable domain framework regions required in order to retain donor mAb binding specificity, as well as the remaining immunoglobulin-derived parts of the antibody chain derived from a human immunoglobulin can be 30 obtained using polynucleotide primers and reverse transcriptase. The CDR-encoding regions are identified using a known database and by comparison to other antibodies.

A rat/human chimeric antibody may then be prepared and assayed for 35 binding ability. Such a chimeric antibody contains the entire non-human donor antibody V<sub>H</sub> and V<sub>L</sub> regions, in association with human Ig constant regions for both chains.

A humanized antibody may be derived from the chimeric antibody, or preferably, made synthetically by inserting the donor mAb CDR-encoding regions from the heavy and light chains appropriately within the selected heavy and light chain framework. Alternatively, a humanized antibody of the invention may be 5 prepared using standard mutagenesis techniques. Thus, the resulting humanized antibody contains human framework regions and donor mAb CDR-encoding regions. There may be subsequent manipulation of framework residues. The resulting humanized antibody can be expressed in recombinant host cells, e.g., COS, CHO or myeloma cells. Other humanized antibodies may be prepared using this 10 technique on other suitable IL-18-specific, neutralizing, high affinity, non-human antibodies.

A conventional expression vector or recombinant plasmid can be produced by placing these coding sequences for the altered antibody in operative association with conventional regulatory control sequences capable of controlling the replication 15 and expression in, and/or secretion from, a host cell. Regulatory sequences include promoter sequences, e.g., CMV promoter, and signal sequences, which can be derived from other known antibodies. Similarly, a second expression vector can be produced having a DNA sequence which encodes a complementary antibody light or heavy chain. Preferably this second expression vector is identical to the first except 20 insofar as the coding sequences and selectable markers are concerned, so to ensure as far as possible that each polypeptide chain is functionally expressed. Alternatively, the heavy and light chain coding sequences for the altered antibody may reside on a single vector.

A selected host cell is co-transfected by conventional techniques with both 25 the first and second vectors (or simply transfected by a single vector) to create the transfected host cell of the invention comprising both the recombinant or synthetic light and heavy chains. The transfected cell is then cultured by conventional techniques to produce the engineered antibody of the invention. The humanized antibody which includes the association of both the recombinant heavy chain and/or 30 light chain is screened from culture by appropriate assay, such as ELISA or RIA. Similar conventional techniques may be employed to construct other altered antibodies and molecules of this invention.

Suitable vectors for the cloning and subcloning steps employed in the methods and construction of the compositions of this invention may be selected by 35 one of skill in the art. For example, the conventional pUC series of cloning vectors, may be used. One vector used is pUC19, which is commercially available from supply houses, such as Amersham (Buckinghamshire, United Kingdom) or

Pharmacia (Uppsala, Sweden). Additionally, any vector which is capable of replicating readily, has an abundance of cloning sites and selectable genes (e.g., antibiotic resistance), and is easily manipulated may be used for cloning. Thus, the selection of the cloning vector is not a limiting factor in this invention.

5       Similarly, the vectors employed for expression of the engineered antibodies according to this invention may be selected by one of skill in the art from any conventional vector. The vectors also contain selected regulatory sequences (such as CMV promoters) which direct the replication and expression of heterologous DNA sequences in selected host cells. These vectors contain the above described DNA  
10      sequences which code for the engineered antibody or altered immunoglobulin coding region. In addition, the vectors may incorporate the selected immunoglobulin sequences modified by the insertion of desirable restriction sites for ready manipulation.

15      The expression vectors may also be characterized by genes suitable for amplifying expression of the heterologous DNA sequences, e.g., the mammalian dihydrofolate reductase gene (DHFR). Other preferable vector sequences include a poly A signal sequence, such as from bovine growth hormone (BGH) and the betaglobin promoter sequence (betaglopro). The expression vectors useful herein may be synthesized by techniques well known to those skilled in this art.

20      The components of such vectors, e.g. replicons, selection genes, enhancers, promoters, signal sequences and the like, may be obtained from commercial or natural sources or synthesized by known procedures for use in directing the expression and/or secretion of the product of the recombinant DNA in a selected host. Other appropriate expression vectors of which numerous types are known in  
25      the art for mammalian, bacterial, insect, yeast, and fungal expression may also be selected for this purpose.

30      The present invention also encompasses a cell line transfected with a recombinant plasmid containing the coding sequences of the engineered antibodies or altered immunoglobulin molecules thereof. Host cells useful for the cloning and other manipulations of these cloning vectors are also conventional. However, most desirably, cells from various strains of *E. coli* are used for replication of the cloning vectors and other steps in the construction of altered antibodies of this invention.

35      Suitable host cells or cell lines for the expression of the engineered antibody or altered antibody of the invention are preferably mammalian cells such as CHO, COS, a fibroblast cell (e.g., 3T3), and myeloid cells, and more preferably a CHO or a myeloid cell. Human cells may be used, thus enabling the molecule to be modified with human glycosylation patterns. Alternatively, other eukaryotic cell lines may be

employed. The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Sambrook *et al.*, cited above.

Bacterial cells may prove useful as host cells suitable for the expression of the recombinant Fabs of the present invention (see, e.g., Plückthun, A., Immunol. Rev., 130:151-188 (1992)). However, due to the tendency of proteins expressed in bacterial cells to be in an unfolded or improperly folded form or in a non-glycosylated form, any recombinant Fab produced in a bacterial cell would have to be screened for retention of antigen binding ability. If the molecule expressed by the bacterial cell was produced in a properly folded form, that bacterial cell would be a desirable host. For example, various strains of *E. coli* used for expression are well-known as host cells in the field of biotechnology. Various strains of *B. subtilis*, *Streptomyces*, other bacilli and the like may also be employed in this method.

Where desired, strains of yeast cells known to those skilled in the art are also available as host cells, as well as insect cells, e.g. *Drosophila* and *Lepidoptera* and viral expression systems. See, e.g. Miller *et al.*, Genetic Engineering, 8:277-298, Plenum Press (1986) and references cited therein.

The general methods by which the vectors of the invention may be constructed, the transfection methods required to produce the host cells of the invention, and culture methods necessary to produce the altered antibody of the invention from such host cell are all conventional techniques. Likewise, once produced, the altered antibodies of the invention may be purified from the cell culture contents according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, gel electrophoresis and the like. Such techniques are within the skill of the art and do not limit this invention.

Yet another method of expression of the humanized antibodies may utilize expression in a transgenic animal, such as described in U.S. Patent No. 4,873,316. This relates to an expression system using the animal's casein promoter which when transgenically incorporated into a mammal permits the female to produce the desired recombinant protein in its milk.

Once expressed by the desired method, the engineered antibody is then examined for *in vitro* activity by use of an appropriate assay. Presently conventional ELISA assay formats are employed to assess qualitative and quantitative binding of the engineered antibody to IL-18. Additionally, other *in vitro* assays may also be used to verify neutralizing efficacy prior to subsequent human clinical studies

performed to evaluate the persistence of the engineered antibody in the body despite the usual clearance mechanisms.

Following the general procedures described for preparing humanized antibodies, one of skill in the art may also construct humanized antibodies from other donor IL-18 antibodies, variable region sequences and CDR peptides described herein. Engineered antibodies can be produced with variable region frameworks potentially recognized as "self" by recipients of the engineered antibody. Minor modifications to the variable region frameworks can be implemented to effect large increases in antigen binding without appreciable increased immunogenicity for the recipient. Such engineered antibodies may effectively treat a human for IL-18 mediated conditions. Such antibodies may also be useful in the diagnosis of such conditions.

#### *VII. Therapeutic/Prophylactic Uses*

This invention also relates to a method of treating humans experiencing autoimmune related symptoms, such as MS, which comprises administering an effective dose of antibodies including one or more of the engineered antibodies or altered antibodies described herein, or fragments thereof.

The therapeutic response induced by the use of the molecules of this invention is produced by the binding to human IL-18 and thus subsequently blocking Th1 stimulation. Thus, the molecules of the present invention, when in preparations and formulations appropriate for therapeutic use, are highly desirable for those persons experiencing autoimmune disease, such as but not limited to MS, RA, IDDM, IBD and psoriasis.

The altered antibodies, antibodies and fragments thereof of this invention may also be used in conjunction with other antibodies, particularly human mAbs reactive with other markers (epitopes) responsible for the condition against which the engineered antibody of the invention is directed.

The therapeutic agents of this invention are believed to be desirable for treatment of autoimmune conditions from about 2 days to 6 months or as needed. For example, longer treatments may be desirable when treating MS or the like. The dose and duration of treatment relates to the relative duration of the molecules of the present invention in the human circulation, and can be adjusted by one of skill in the art depending upon the condition being treated and the general health of the patient.

The mode of administration of the therapeutic agent of the invention may be any suitable route which delivers the agent to the host. The altered antibodies, antibodies, engineered antibodies, and fragments thereof, and pharmaceutical

compositions of the invention are particularly useful for parenteral administration, i.e., subcutaneously, intramuscularly, intravenously, or intranasally.

Therapeutic agents of the invention may be prepared as pharmaceutical compositions containing an effective amount of the engineered (e.g., humanized) antibody of the invention as an active ingredient in a pharmaceutically acceptable carrier. In the prophylactic agent of the invention, an aqueous suspension or solution containing the engineered antibody, preferably buffered at physiological pH, in a form ready for injection is preferred. The compositions for parenteral administration will commonly comprise a solution of the engineered antibody of the invention or a cocktail thereof dissolved in an pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be employed, e.g., 0.4% saline, 0.3% glycine, and the like. These solutions are sterile and generally free of particulate matter. These solutions may be sterilized by conventional, well known sterilization techniques (e.g., filtration). The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, etc. The concentration of the antibody of the invention in such pharmaceutical formulation can vary widely, i.e., from less than about 0.5%, usually at or at least about 1% to as much as 15 or 20% by weight and will be selected primarily based on fluid volumes, viscosities, etc., according to the particular mode of administration selected.

Thus, a pharmaceutical composition of the invention for intramuscular injection could be prepared to contain 1 mL sterile buffered water, and between about 1 ng to about 100 mg, e.g. about 50 ng to about 30 mg or more preferably, about 5 mg to about 25 mg, of an engineered antibody of the invention. Similarly, a pharmaceutical composition of the invention for intravenous infusion could be made up to contain about 250 ml of sterile Ringer's solution, and about 1 to about 30 and preferably 5 mg to about 25 mg of an engineered antibody of the invention. Actual methods for preparing parenterally administrable compositions are well known or will be apparent to those skilled in the art and are described in more detail in, for example, Remington's Pharmaceutical Science, 15th ed., Mack Publishing Company, Easton, Pennsylvania.

It is preferred that the therapeutic agent of the invention, when in a pharmaceutical preparation, be present in unit dose forms. The appropriate therapeutically effective dose can be determined readily by those of skill in the art.

To effectively treat an inflammatory disorder in a human or other animal, one dose of approximately 0.1 mg to approximately 20 mg per 70 kg body weight of a protein or an antibody of this invention should be administered parenterally, preferably *i.v.*

or i.m. (intramuscularly). Such dose may, if necessary, be repeated at appropriate time intervals selected as appropriate by a physician during the disease.

The altered antibodies and engineered antibodies of this invention may also be used in diagnostic regimens, such as for the determination of IL-18 mediated disorders or tracking progress of treatment of such disorders. As diagnostic reagents, these altered antibodies may be conventionally labeled for use in ELISA's and other conventional assay formats for the measurement of IL-18 levels in serum, plasma or other appropriate tissue, or the release by human cells in culture. The nature of the assay in which the altered antibodies are used are conventional and do not limit this disclosure.

Thus, one embodiment of the present invention relates to a method for aiding the diagnosis of autoimmune disease and other conditions associated with excess Th1 T cell production in a patient which comprises the steps of determining the amount of human IL-18 in sample (plasma or tissue) obtained from said patient and comparing said determined amount to the mean amount of human IL-18 in the normal population, whereby the presence of a significantly elevated amount of IL-18 in the patient's sample is an indication autoimmune disease and other conditions associated with excess Th1 T cell production.

The antibodies, altered antibodies or fragments thereof described herein can be lyophilized for storage and reconstituted in a suitable carrier prior to use. This technique has been shown to be effective with conventional immunoglobulins and art-known lyophilization and reconstitution techniques can be employed.

The following examples illustrate various aspects of this invention including the construction of exemplary engineered antibodies and expression thereof in suitable vectors and host cells, and are not to be construed as limiting the scope of this invention. All amino acids are identified by conventional three letter or single letter codes. All necessary restriction enzymes, plasmids, and other reagents and materials were obtained from commercial sources unless otherwise indicated. All general cloning legation and other recombinant DNA methodology were as performed in T. Maniatis *et al.*, cited above, or the second edition thereof (1989), eds. Sambrook *et al.*, by the same publisher ("Sambrook *et al.*").

#### Example 1 - Production of MAbs to IL-18

##### A. *Monoclonal antibody generation*

Mice (F1 hybrids of Balb/c and C57BL/6) or rats (Sprague Dawley) were immunised with 30 µg recombinant IL-18 in adjuvant and 4 weeks later with 30 µg

IL-18 in adjuvant. On the basis of a good serum antibody titre to IL-18 animals received a further immunization of 10-30 µg IL-18 (i.p. in saline). Three days following the final immunization a splenectomy was performed. Mouse or rat spleen cells were used to prepare hybridomas by standard procedures. (Zola, H.Ed.,  
5 Monoclonal Antibodies. CRC Press Inc. 1987). Positive hybridomas were cloned by the limiting dilution method.

*B. Purification of Mabs*

Mabs were purified by ProsepA (Bio Processing, Consett, UK) chromatography respectively using the manufacturer's instructions. Mabs were  
10 >95% pure by SDS-PAGE.

*C. Isotyping of Mabs*

All rat and mouse Mabs were isotype by commercially available kits (Zymed, Amersham) and found to be IgG1 kappa.  
15

**Example 2 – Assays**

*A. Biotinylation Of IL-18*

IL-18 was biotinylated using a kit purchased from Molecular Probes Inc. using a 10:1 ratio of biotinylation reagent. Biotinylation had no effect on the  
20 biological activity of IL-18

*B. Hybridoma Screening Assay*

96-well plates were coated with streptavidin (2µg/ml, 100µl/well in PBS) by incubation overnight at 4°C. The solution was then aspirated and non-specific  
25 binding sites were blocked with 250µl/well of 1% bovine serum albumin (BSA) in TBS buffer (50mM Tris, 150 mM NaCl, 0.02% Kathon, pH 7.4) for 5-60 minutes at RT. Following this and each of the following steps, the plate was washed 4 times in wash buffer (10 mM Tris, 150 mM NaCl, 0.05% Tween 20, 0.02% Kathon, pH 7.4). To each well, 100 µL biotin IL-18 (100ng/ml) in assay buffer (0.5% BSA, 0.05%  
30 bovine gamma globulin, 0.01% Tween 40, 20µM diethylenetriaminepentaacetic in TBS buffer) was added and the plates were incubated for 30 min at RT in a shaker-incubator. To each well 50µl hybridoma medium and 50 µl assay buffer was then

added and incubated for 60 min at RT in a shaker-incubator. To each well was then added 100ul 0.5 $\mu$ g/ml Eu<sup>3+</sup> labelled anti-mouse or anti-rat antibody in assay buffer. Finally 200  $\mu$ l /well of enhancer (Wallac) was added and incubated for 5 min at RT and the time-resolved fluorescence measured. Hybridomas having counts >100K  
5 were expanded into 24-well plates.

*C. Immunoassay*

To determine the specificity of the anti-IL-18 Mabs) generated 96-well plates were coated, blocked and incubated with biotin IL-18 as above. All the following  
10 incubations were performed in a shaker-incubator at RT. After washing the wells 50  $\mu$ l IL-18 (3  $\mu$ g/ml) or assay buffer and 50  $\mu$ l Mab were added and incubated for 60 min. After washing the wells 100ul 0.5 $\mu$ g/ml Eu<sup>3+</sup> labelled anti-mouse or anti-rat antibody in assay buffer was added for 60 min, the wells washed and then 100  $\mu$ l /well of enhancer (Wallac) was added and incubated for 5 min at RT and the time-  
15 resolved fluorescence measured. All positive hybridomas showed displacement of binding with IL-18.

*D. Neutralization Assay*

PBMC from healthy donors were isolated by Ficol-Paque (Pharmacia)  
20 gradient and cultured in 96 well plates in 10% FBS DMEM/F12 media with 1 $\mu$ g/ml ConA (Sigma) in the presence of IL-18 (5ng/ml) and/or Mabs. After 18h culture at 37°C, 5% CO<sub>2</sub> in air, 90% humidity 25 $\mu$ l media was removed and interferon gamma (IFNg) concentration measured by immunoassay. The results, obtained from an average of three experiments, are summarized in Table I.  
25

*E. Affinity Measurements Of Monoclonal Antibody*

The affinity of the purified mAbs was measured in the BIACore optical biosensor (Pharmacia Biosensor, Uppsala, Sweden) using a flow rate of 30ul/min.  
30 Kinetic data was evaluated using relationships described previously (Karlsson et al, J. Immunol. Meth., 145:229-240 (1991) and which is incorporated by reference in its entirely. The mAb (diluted in HBS buffer, 10 mM HEPES, 150 mM NaCl, 0.01%

Tween-20, pH 7.4) was injected over a rabbit anti-mouse IgG Fc or goat anti-rat IgG Fc surface, followed by buffer flow and the RU was recorded. IL-18 (diluted in HBS buffer) was then injected for 180 seconds followed by a buffer flow for 500 seconds and the RU was recorded. The sensor chip surface was regenerated by an injection of 5 0.1 M phosphoric acid. The on-rates (Kass) and off-rates (Kdiss) of binding were calculated using BIACore software and together these yield a calculated equilibrium constant ( $K_D$ ) of  $12 \times 10^{-9}$  M for mAb 13G9,  $3.9 \times 10^{-11}$  M for mAb 2C10 and  $1.5 \times 10^{-10}$  M for mAb 14B7. See Table I.

10    *F. Epitope Analysis Of Monoclonal Antibody*

The epitope analysis of the purified Mabs was measured in the BIACore. Using a flow rate of 10 $\mu$ l/min, the first Mab (diluted in HBS buffer) was injected over a rabbit anti-mouse IgG Fc or goat anti-rat IgG Fc surface, followed by an injection of IL-18 for 240s, an injection of blocking Mabs for 48s and an injection of 15 the second Mab for 240s. The surface was regenerated by an injection of 0.1M phosphoric acid and the RU was recorded after each injection. It was found that Mabs 13G9, 2C10 and 14B7 have similar or overlapping epitopes.

TABLE I

20    Affinity and neutralizing activity of mAbs reactive with human IL-18

mAb	Kd (pM) <sup>a</sup>	Neutralisation IC50 (nM) <sup>b</sup>
2C10 (rat)	39	0.1
25    14B7 (rat)	150	0.2
13G9 (mouse)	12000	3.0

<sup>a</sup> Determined by optical biosensor (BIACore) analysis (25°C)

<sup>b</sup> Inhibition of IFN gamma production (in nM) of PBMC in response to 5ng/ml human IL-18

Example 3 – CDR sequences*Gene Cloning and Sequence Analysis:*

The variable heavy and light genes were cloned from hybridoma cells using  
5 standard molecular biological methods described briefly as follows. Total RNA was  
isolated from the hybridoma cells using TRIzol Reagent (Life Technologies Cat. #  
15596-026) according to manufacturer's protocol. The RNA was reverse transcribed  
with a RT-PCR kit per the manufacturer's instructions (Boehringer Mannheim Cat.  
No. 1483-188) using a poly-dT oligonucleotide for priming. Following first strand  
10 cDNA synthesis, the heavy and light V regions were PCR amplified using 3'  
constant region specific primers and degenerate 5' primers. The degenerate 5' primer  
sequences were designed to encode the previously determined N terminal amino acid  
sequences of the variable heavy or light chain regions. Full length sequences from  
multiple clones were obtained from each PCR amplification and aligned to provide  
15 consensus. Accordingly, the first 17 bases of DNA sequence for both the heavy and  
light chains are PCR primer generated, however the translated protein sequence is  
native.

The nucleotide and deduced amino acid sequences for hybridoma antibodies  
2C10, 13G9, and 14B7 are shown Figures 1-6. In each case the CDR s and the  
20 nucleotide sequences encoding them are *boxed*. The degenerate primer sequences  
are *bolded*.

**WHAT IS CLAIMED IS:**

1. A rodent neutralizing monoclonal antibody specific for human interleukin-18 and having a binding affinity characterized by a dissociation constant equal to or less than about  $3.9 \times 10^{-11}$  M.
2. The monoclonal antibody according to claim 1 which is a rat monoclonal antibody.  
10
3. The monoclonal antibody according to claim 1 which is a murine monoclonal antibody.
4. The monoclonal antibody according to claim 2 which comprises the light chain amino acid sequence of SEQ ID NO: 1, and the heavy chain amino acid sequence of SEQ ID NO: 9.  
15
5. The monoclonal antibody according to claim 3 which comprises the light chain amino acid sequence of SEQ ID NO: 17 and the heavy chain amino acid sequence of SEQ ID NO: 25.  
20
6. The monoclonal antibody according to claim 2 which comprises the light chain amino acid sequence of SEQ ID NO: 33 and the heavy chain amino acid sequence of SEQ ID NO: 41.  
25
7. The monoclonal antibody according to claim 1 having the identifying characteristics of 2C10, 14B7 or 13G9.
8. A hybridoma which produces the monoclonal antibody of claim 4.  
30
9. A hybridoma which produces the monoclonal antibody of claim 5.
10. A hybridoma which produces the monoclonal antibody of claim 6.  
35
11. A hybridoma having the identifying characteristics of cell line 19522C10(2)F2(1)A1, 195214B7(1)H10 and 187413G9(3)F12

12. A neutralizing Fab fragment or F(ab')<sub>2</sub> fragment thereof, produced by deleting the Fc region of the monoclonal antibody of claim 1.

5 13. An altered antibody comprising a heavy chain and a light chain, wherein the framework regions of said heavy and light chains are derived from at least one selected antibody and the amino acid sequences of the complementarity determining regions of each said chain are derived from the monoclonal antibody of claim 1.

10

14. An immunoglobulin light chain complementarity determining region (CDR), the amino acid sequence of which is selected from the group consisting of:

- (a) SEQ ID NO: 3
- (b) SEQ ID NO: 5
- 15 (c) SEQ ID NO: 7
- (d) SEQ ID NO: 19
- (e) SEQ ID NO: 21
- (f) SEQ ID NO: 23
- (g) SEQ ID NO: 35
- 20 (h) SEQ ID NO: 37
- (i) SEQ ID NO: 39

15. An immunoglobulin heavy chain complementarity determining region (CDR), the amino acid sequence of which is selected from the group consisting of:

- (a) SEQ ID NO: 11
- (b) SEQ ID NO: 13
- (c) SEQ ID NO: 15
- (d) SEQ ID NO: 27
- 30 (e) SEQ ID NO: 29
- (f) SEQ ID NO: 31
- (g) SEQ ID NO: 43
- (h) SEQ ID NO: 45
- (i) SEQ ID NO: 47

35

16. A nucleic acid molecule encoding the immunoglobulin complementarity determining region (CDR) of claim 14.

17. A nucleic acid molecule encoding the immunoglobulin complementarity determining region (CDR) of claim 15.

5 18. A pharmaceutical composition comprising the altered antibody of claim 13 and a pharmaceutically acceptable carrier.

10 19. A method of treating conditions associated with autoimmune disease comprising the step of administering to said human in need thereof an effective amount of the altered antibody of claim 13.

20. The method of claim 19 where said disease is multiple sclerosis.

15 21. The method of claim 19 where said disease is rheumatoid arthritis type I or insulin dependent diabetes.

20 22. The method of claim 19 where said disease is inflammatory bowel disease.

23. The method of claim 19 where said disease is psoriasis.

24. An isolated nucleic acid sequence which is selected from the group consisting of:

25 (a) a nucleic acid sequence encoding the altered antibody of claim 13  
(b) a nucleic acid sequence complementary to (a); and  
(c) a fragment or analog of (a) or (b), which encodes a protein,  
characterized by having a specificity for human interleukin-18;  
wherein said sequence optionally contains a restriction site.

30 25. A method to assess the presence or absence of human IL-18 in a

human which comprises obtaining a sample of biological fluid from a patient and allowing the monoclonal antibody of claim 1 to come in contact with such sample under conditions such that an IL-18/monoclonal antibody complex can form and detecting the presence or absence of said IL-18/monoclonal antibody complex.

26. A method for aiding in the diagnosis of autoimmune disease associated with comprising the steps of determining the amount of human IL-18 in a sample of a patient according to the method of claim 25 and comparing that to the mean amount of human IL-18 in the normal population, whereby the presence of  
5 significantly elevated amount of human IL-18 in the patient is an indication of autoimmune disease.

V<sub>k</sub>2c10

1   D   I   Q   M   T   Q   S   P   A   S   L   S   A   S   L   15  
**GAC ATT CAA ATG ACC CAG** TCT CCA GCT TCC CTG TCT GCA TCT CTG  
 CTG TAA GTT TAC TGG GTC AGA GGT CGA AGG GAC AGA CGT AGA GAC

**CDRI**

16   G   E   T   V   S   I   E   C   L   A   S   E   D   I   Y   90  
 GGA GAA ACT GTC TCC ATC GAA TGT CTG GCA AGT GAG GAC ATA TAC  
 CCT CTT TGA CAG AGG TAG CTT ACA GAC CGT TCA CTC CTG TAT ATG   30

31   T   Y   L   T   W   Y   Q   Q   K   P   G   K   S   P   Q   45  
 ACT TAT TTA ACA TGG TAT CAG CAG AAA CCA GGG AAA TCT CCT CAA  
 TGA ATA AAT TGT ACC ATA GTC GTC TTT GGT CCC TTT AGA GGA GTT

**CDRII**

46   L   L   I   Y   150   1   70  
 CTC CTG ATC TAT GGT GCA AAT AAG TTG CAA GAT GGG GTC CCA TCA  
 GAG GAC TAG ATA CCA CGT TTA TTC AAC GTT CTA CCC CAG GGT AGT   60

61   R   F   S   G   S   G   S   G   T   Q   Y   S   L   K   I   75  
 CGG TTC AGT GGC AGT GGA TCT GGC ACA CAG TAT TCT CTC AAG ATC  
 GCC AAG TCA CCG TCA CCT AGA CCG TGT GTC ATA AGA GAG TTC TAG

76   2   30   25   0   270  
 S   G   I   Q   P   E   D   E   G   D   Y   F   C   L   Q   90  
 AGC GGC ATA CAA CCT GAA GAT GAA GGG GAT TAT TTC TGT CTA CAG  
 TCG CCG TAT GTT GGA CTT CTA CTT CCC CTA ATA AAG ACA GAT GTC

**CDRIII**

91   2   90   31   0   105  
 G   S   K   F   P   L   T   F   G   S   G   T   K   L   E   105  
 GGT TCC AAG TTT CCG CTC ACG TTC GGT TCT GGG ACC AAG CTG GAG  
 CCA AGG TTC AAA GGC GAG TGC AAG CCA AGA CCC TGG TTC GAC CTC

106   I   K   R   108  
 ATC AAA CGG  
 TAG TTT GCC

**FIGURE 1**

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## VH2C10

1    E    V    Q    L    Q    Q    S    G    A    E    L    V    R    P    G    15  
**GAG GTC CAG CTA CAG CAG** TCT GGG GCT GAG CTT GTG AGA CCT GGG  
 CTC CAG GTC GAT GTC AGA CCC CGA CTC GAA CAC TCT GGA CCC

16    T    S    V    K    L    S    C    K    V    S    G    E    I    S    T    30  
 ACC TCT GTG AAG TTA TCT TGC AAA GTT TCT GGC GAA ATA AGT ACA  
 TGG AGA CAC TTC AAT AGA ACG TTT CAA AGA CCG CTT TAT TCA TGT

## CDRI

31    **G    Y    Y    F    H**    F    V    R    R    R    P    G    Q    G    L    45  
 GGA TAC TAT TTC CAC TTT GTG AGG CGA AGG CCT GGA CAG GGT CTG  
 CCT ATG ATA AAG GTG AAA CAC TCC GCT TCC GGA CCT GTC CCA GAC

## CDRII

46    E    W    I    G    **R    I    D    P    E    D    D**    150    1    70    60  
 GAA TGG ATA GGA AGG ATT GAT CCT GAG GAT GAT AGT ACT AAA TAT  
 CTT ACC TAT CCT TCC TAA CTA GGA CTC CTA CTA TCA TGA TTT ATA

61    **A    E    R    F    K    D**    R    A    T    L    T    A    Q    T    S    75  
 GCT GAG AGG TTC AAA GAC AGG GCG ACG CTC ACT GCA CAA ACA TCC  
 CGA CTC TCC AAG TTT CTG TCC CGC TGC GAG TGA CGT GTT TGT AGG

76    **S    N    T    A    Y    L    N    L    S    S    L    T    S    E    D**    230    250    270    90  
 TCC AAC ACA GCC TAC CTG AAC CTC AGC AGC CTG ACC TCT GAG GAC  
 AGG TTG TGT CGG ATG GAC TTG GAG TCG TCG GAC TGG AGA CTC CTG

91    T    A    T    Y    F    C    T    T    **W    R    I    Y    R    D    S**    290    310    105  
 ACT GCA ACT TAT TTT TGT ACC ACA TGG CGG ATA TAC CGA GAT AGT  
 TGA CGT TGA ATA AAA ACA TGG TGT ACC GCC TAT ATG GCT CTA TCA

## CDRIII

106    **S    G    R    P    F    Y    V    M    D    A**    330    3    50    120  
 TCT GGC CGC CCC TTC TAT GTT ATG GAT GCC TGG GGT CAA GGA GCT  
 AGA CCG GCG GGG AAG ATA CAA TAC CTA CGG ACC CCA GTT CCT CGA

121    **S    V    T    V    S    S**    370    126  
 TCA GTC ACT GTC TCC TCA  
 AGT CAG TGA CAG AGG AGT

## FIGURE 2

### 2/6

Vk13g9

1	D	V	V	M	T	Q	T	P	L	S	L	P	V	S	L	15
<b>GAC</b>	<b>GTT</b>	<b>GTT</b>	<b>ATG</b>	<b>ACT</b>	<b>CAA</b>	ACT	CCT	CTC	TCC	CTG	CCT	GTC	AGT	CTT		
CTG	CAA	CAA	TAC	TGA	GTT	TGA	GGA	GAG	AGG	GAC	GGA	CAG	TCA	GAA		

CDR I

	CDR 1														
	50					70					90				
16	G	D	Q	A	S	I	S	C	R	S	S	Q	S	L	V
	GGA	GAT	CAA	GCC	TCC	ATC	TCT	TGC	AGA	TCT	AGT	CAG	AGC	CTT	GTA
	CCT	CTA	GTT	CGG	AGG	TAG	AGA	ACG	TCT	AGA	TCA	GTC	TCG	GAA	CAT

	1 10										13 0							
31	H	S	N	G	N	T	Y	L	H		W	Y	L	Q	K	P	45	
	CAC	AGT	AAT	GGA	AAC	ACC	TAT	TTA	CAT	TGG	TAC	CTG	CAG	AAG	CCA			
	GTG	TCA	TTA	CCT	TTG	TGG	ATA	AAT	GTA	ACC	ATG	GAC	GTC	TTC	GGT			

CDR II

CDR II																
46	150											60				
	G	Q	S	P	K	L	L	I	Y	K	V	S	N	R	F	
	GGC	CAG	TCT	CCA	AAG	CTC	CTG	ATC	TAC	AAA	GTT	TCC	AAC	CGA	TTT	
	CCG	GTC	AGA	GGT	TTC	GAG	GAC	TAG	ATG	TTT	CAA	AGG	TTG	GCT	AAA	

61	<span style="border: 1px solid black; padding: 2px;">S</span> G V P D R F S G S G S G T D	210	75
	TCT GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGT ACA GAT		
	AGA CCC CAG GGT CTG TCC AAG TCA CCG TCA CCT AGT CCA TGT CTA		

2 30	25 0	270
76 F T L K I S R V E A E D L G V		90
TTC ACA CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT		
AAG TGT GAG TTC TAG TCG TCT CAC CTC CGA CTC CTA GAC CCT CAA		

CDR III

	2 90										31 0					
91	Y	F	C	S	Q	S	T	H	V	P	P	Y	T	F	G	105
TAT	TTC	TGC	TCT	CAA	AGT	ACA	CAT	GTT	CCT	CCG	TAC	ACG	TTC	GGA		
ATA	AAG	ACG	AGA	GTT	TCA	TGT	GTA	CAA	GGA	GGC	ATG	TGC	AAG	CCT		

330		
106	G      G      T      K      L      E      I      K      R	114
	GGG    GGG    ACC    AAG    CTG    GAA    ATA    AAA    CGG	
	CCC    CCC    TGG    TTC    GAC    CTT    TAT    TTT    GCC	

**FIGURE 3**  
**3/6**

VH13G9

**FIGURE 4**  
**4/6**

Vk14B7

1	D	I	Q	M	T	Q	S	P	A	S	L	S	A	S	L	15
<b>GAT</b>	<b>ATT</b>	<b>CAA</b>	<b>ATG</b>	<b>ACG</b>	<b>CAG</b>	TCT	CCA	GCT	TCC	CTG	TCT	GCA	TCT	CTG		
CTA	TAA	GTT	TAC	TGC	GTC	AGA	GGT	CGA	AGG	GAC	AGA	CGT	AGA	GAC		

	50								70								CDR I								90																				
16	G	E	T	V	S	I	E	C	L	A	S	E	D	I	Y	GGA	GAA	ACT	GTC	TCC	ATC	GAA	TGT	CTA	GCA	AGT	GAG	GAC	ATA	TAC	CCT	CTT	TGA	CAG	AGG	TAG	CTT	ACA	GAT	CGT	TCA	CTC	CTG	TAT	ATG

31	S	Y	L	A	W	Y	Q	Q	K	P	G	K	S	P	Q	45
	AGT	TAT	TTA	GCA	TGG	TAT	CAA	CAG	AAG	CCA	GGG	AAA	TCT	CCT	CAG	
	TCA	ATA	AAT	CGT	ACC	ATA	GTT	GTC	TTC	GGT	CCC	TTT	AGA	GGA	GTC	

150      **CDR II**

46	L	L	I	Y	A	T	K	R	L	Q	D	G	V	P	S	60
	CTC	CTG	ATC	TAT	GCC	ACA	AAA	AGG	TTG	CAA	GAT	GGG	GTC	CCA	TCA	
	GAG	GAC	TAG	ATA	CGG	TGT	TTT	TCC	AAC	GTT	CTA	CCC	CAG	GGT	AGT	

61	190														210				
	R	F	S	G	S	G	S	G	T	Q	Y	S	L	K	I	75			
	CGG	TTC	AGT	GGC	AGT	GGA	TCT	GGC	ACA	CAG	TAT	TCT	CTC	AAA	ATA				
	GCC	AAG	TCA	CCG	TCA	CCT	AGA	CCG	TGT	GTC	ATA	AGA	GAG	TTT	TAT				

76	2	30							25	0								270		90
	S	D	M	Q	P	E	D	E	G	D	Y	F	C	L	Q					
	AGC	GAC	ATG	CAA	CCT	GAA	GAT	GAA	GGG	GAT	TAT	TTC	TGT	CTA	CAG					
	TCG	CTG	TAC	GTT	GGA	CTT	CTA	CTT	CCC	CTA	ATA	AAG	ACA	GAT	GTC					

CDR III							2 90							31 0						
N	S	K	F	P	V	T	F	G	S	G	T	K	L	E	105					
AAT	TCC	AAG	TTT	CCG	GTC	ACG	TTC	GGT	TCT	GGG	ACC	AAG	CTG	GAG						
TTA	AGG	TTC	AAA	GGC	CAG	TGC	AAG	CCA	AGA	CCC	TGG	TTC	GAC	CTC						

106	I	K	R	108
	ATC	AAA	CGG	
	TAG	TTT	GCC	

# **FIGURE 5**

## **5/6**

VH14B7

## **FIGURE 6**

**6/6**

## SEQUENCE LISTING

<110> Holmes, Stephen D.  
Ho, Yen Sen  
Taylor, Alexander  
Abdel-Meguid, Sherin S.

<120> Recombinant IL-18 Antagonists Useful in  
Treatment of IL-18 Mediated Disorders

<130> P50897

<140> 60/125,299  
<141> 1999-03-19

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1 5 10 15

gaa act gtc tcc atc gaa tgt ctg gca agt gag gac ata tac act tat 96  
Glu Thr Val Ser Ile Glu Cys Leu Ala Ser Glu Asp Ile Tyr Thr Tyr  
20 25 30

tta aca tgg tat cag cag aaa cca ggg aaa tct cct caa ctc ctg atc 144  
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile  
           35                40                45

tat ggt gca aat aag ttg caa gat ggg gtc cca tca cgg ttc agt ggc 192  
 Tyr Gly Ala Asn Lys Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly  
       50                  55                  60

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agt gga tct ggc aca cag tat tct ctc aag atc agc ggc ata caa cct      240
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Ser Gly Ile Gln Pro
   65           70           75           80

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gaa gat gaa ggg gat tat ttc tgt cta cag ggt tcc aag ttt ccg ctc      288  
 Glu Asp Glu Gly Asp Tyr Phe Cys Leu Gln Gly Ser Lys Phe Pro Leu  
                   85                    90                    95

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acg ttc ggt tct ggg acc aag ctg gag atc aaa cg
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
          100           105

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1				5					10				15		
Glu	Thr	Val	Ser	Ile	Glu	Cys	Leu	Ala	Ser	Glu	Asp	Ile	Tyr	Thr	Tyr
				20					25				30		
Leu	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Ile
				35				40				45			
Tyr	Gly	Ala	Asn	Lys	Leu	Gln	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
				50			55				60				
Ser	Gly	Ser	Gly	Thr	Gln	Tyr	Ser	Leu	Lys	Ile	Ser	Gly	Ile	Gln	Pro
65				70					75				80		
Glu	Asp	Glu	Gly	Asp	Tyr	Phe	Cys	Leu	Gln	Gly	Ser	Lys	Phe	Pro	Leu
				85				90				95			

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg  
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Leu Ala Ser Glu Asp Ile Tyr Thr Tyr Leu Thr  
1 5 10

33

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1 5

21

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1 5

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1 5

27

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1 5

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 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr  
 1 5 10 15

tct gtg aag tta tct tgc aaa gtt tct ggc gaa ata agt aca gga tac 96  
 Ser Val Lys Leu Ser Cys Lys Val Ser Gly Glu Ile Ser Thr Gly Tyr  
 20 25 30

tat ttc cac ttt gtg agg cga agg cct gga cag ggt ctg gaa tgg ata 144  
 Tyr Phe His Phe Val Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

gga agg att gat cct gag gat gat agt act aaa tat gct gag agg ttc 192  
 Gly Arg Ile Asp Pro Glu Asp Asp Ser Thr Lys Tyr Ala Glu Arg Phe  
 50 55 60

aaa gac agg gcg acg ctc act gca caa aca tcc tcc aac aca gcc tac 240  
 Lys Asp Arg Ala Thr Leu Thr Ala Gln Thr Ser Ser Asn Thr Ala Tyr  
 65 70 75 80

ctg aac ctc agc agc ctg acc tct gag gac act gca act tat ttt tgt 288  
 Leu Asn Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys  
 85 90 95

acc aca tgg cgg ata tac cga gat agt tct ggc cgc ccc ttc tat gtt 336  
 Thr Thr Trp Arg Ile Tyr Arg Asp Ser Ser Gly Arg Pro Phe Tyr Val  
 100 105 110

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 115 120 125

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&lt;211&gt; 126

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1 5 10 15

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20 25 30

Tyr Phe His Phe Val Arg Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Arg Ile Asp Pro Glu Asp Asp Ser Thr Lys Tyr Ala Glu Arg Phe  
50 55 60

Lys Asp Arg Ala Thr Leu Thr Ala Gln Thr Ser Ser Asn Thr Ala Tyr  
65 70 75 80

Leu Asn Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95

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100 105 110

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115 120 125

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Gly Tyr Tyr Phe His  
1 5

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Gly Tyr Tyr Phe His

1 5

<210> 13

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1 5 10 15

gac

48

51

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1 5 10 15

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1 5 10 15

gcc 51

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Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly  
1 5 10 15

gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt gta cac agt 96  
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser  
20 25 30

aat gga aac acc tat tta cat tgg tac ctg cag aag cca ggc cag tct 144  
Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca 192  
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro  
50 55 60

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gac agg ttc agt ggc agt gga tca ggt aca gat ttc aca ctc aag atc 240
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65           70           75           80

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Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85           90           95

aca cat gtt cct ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata 336
Thr His Val Pro Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile
100          105          110

aaa cg
Lys Arg 342

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   20          25                   30
Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
   35          40                   45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
   50          55                   60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
   65          70                   75                  80
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
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Thr His Val Pro Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
  100         105                  110
Lys Arg

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<210> 19  
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<223> VK13G9 Light Chain CDR I

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<212> PRT  
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<210> 23

<211> 30

<212> DNA

<213> Mus musculus

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<223> CK13G9 Light chain CDR III

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<210> 24

<211> 10

<212> PRT

<213> Mus musculus

<400> 24

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<210> 25

<211> 369

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(369)

<223> Heavy chain V region

<400> 25

caa gtt act ctt aag gag tct ggc cct ggg ata ttg aag ccc tca cag			48
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln			
1	5	10	15
acc ctc agt ctg act tgt tct ttc tct ggg ttt tct ctg agc act tct			96
Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser			
20	25	30	
ggt atg ggt att gcc tgg gtt cgt cag cct tca ggg aag ggt ctg gag			144
Gly Met Gly Ile Ala Trp Val Arg Gln Pro Ser Gly Lys Gly Leu Glu			
35	40	45	
tgg ctg gca gac att tgg tgg gat gat aat aag tat tat aat cca tcc			192
Trp Leu Ala Asp Ile Trp Trp Asp Asp Asn Lys Tyr Tyr Asn Pro Ser			
50	55	60	
ctg gag agc cag ctc aca atc tcc aag gat acc tcc aga aac cag gta			240
Leu Glu Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val			
65	70	75	80
ttc ctc acg atc acc agt gtg gac act gca gat tct gcc act tat tac			288
Phe Leu Thr Ile Thr Ser Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr			
85	90	95	
tgt gct cgt cat cat tac gac ggt agt agc ctc ctg cct atg gac tac			336
Cys Ala Arg His His Tyr Asp Gly Ser Ser Leu Leu Pro Met Asp Tyr			
100	105	110	
tgg ggt caa gga acc tca gtc acc gtc tcc tca			369
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser			
115	120		
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Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser			
12/21			

20	25	30
Gly Met Gly Ile Ala Trp Val Arg Gln Pro Ser Gly Lys Gly Leu Glu		
35	40	45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Asn Lys Tyr Tyr Asn Pro Ser		
50	55	60
Leu Glu Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val		
65	70	75
Phe Leu Thr Ile Thr Ser Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr		
85	90	95
Cys Ala Arg His His Tyr Asp Gly Ser Ser Leu Leu Pro Met Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser		
115	120	

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21

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48

<210> 30

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<212> PRT

<213> Mus musculus

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<212> DNA

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<223> VH13G9 Heavy chain CDR III

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39

<210> 32

<211> 13

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<213> Mus musculus

&lt;400&gt; 32

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 1                   5                   10

&lt;210&gt; 33

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(324)

&lt;223&gt; Light chain V region

&lt;400&gt; 33

gat att caa atg acg cag tct cca gct tcc ctg tct gca tct ctg gga  
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 1                   5                   10                   15

48

gaa act gtc tcc atc gaa tgt cta gca agt gag gac ata tac agt tat  
 Glu Thr Val Ser Ile Glu Cys Leu Ala Ser Glu Asp Ile Tyr Ser Tyr  
 20                   25                   30

96

tta gca tgg tat caa cag aag cca ggg aaa tct cct cag ctc ctg atc  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile  
 35                   40                   45

144

tat gcc aca aaa agg ttg caa gat ggg gtc cca tca cgg ttc agt ggc  
 Tyr Ala Thr Lys Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly  
 50                   55                   60

192

agt gga tct ggc aca cag tat tct ctc aaa ata agc gac atg caa cct  
 Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Ser Asp Met Gln Pro  
 65                   70                   75                   80

240

gaa gat gaa ggg gat tat ttc tgt cta cag aat tcc aag ttt ccg gtc  
 Glu Asp Glu Gly Asp Tyr Phe Cys Leu Gln Asn Ser Lys Phe Pro Val  
 85                   90                   95

288

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324

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				20					25					30	
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Ile
				35			40					45			
Tyr	Ala	Thr	Lys	Arg	Leu	Gln	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
				50			55				60				
Ser	Gly	Ser	Gly	Thr	Gln	Tyr	Ser	Leu	Lys	Ile	Ser	Asp	Met	Gln	Pro
				65			70			75			80		
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<210> 37

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<223> CK14B7 Light chain CDR II

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21

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1 5

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<211> 7

<212> PRT

<213> Rattus norvegicus

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<213> Rattus norvegicus

<220>

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<223> VK14B7 Light chain CDR III

<400> 39

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1 5 10 15	

tct gtg aag ttt tct tgc aaa gtt tct ggc gat acc cct aca aca tac	96
Ser Val Lys Phe Ser Cys Lys Val Ser Gly Asp Thr Pro Thr Thr Tyr	
20 25 30	

tac gtg cac ttt gtg aga caa agg cct gga cag ggt ctg gaa tgg ata	144
Tyr Val His Phe Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	

gga agg att gat cct gag gat act agt act aaa tat gct gag aag ttc	192
Gly Arg Ile Asp Pro Glu Asp Thr Ser Thr Lys Tyr Ala Glu Lys Phe	
50 55 60	

aga aat aag gcg aca ttc act gca gat cca tcc tcc aac aca gcc tac	240
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Arg Asn Lys Ala Thr Phe Thr Ala Asp Pro Ser Ser Asn Thr Ala Tyr				
65	70	75	80	
ct aac ctc agc agc ctg acc cct gag gac act gca acc tat ttt tgt				288
Leu Asn Leu Ser Ser Leu Thr Pro Glu Asp Thr Ala Thr Tyr Phe Cys				
85	90	95		
acc ata atg cgg tac cat agt acc tat agg gtc tat gtt atg gat ttc				336
Thr Ile Met Arg Tyr His Ser Thr Tyr Arg Val Tyr Val Met Asp Phe				
100	105	110		
tgg ggt caa gga act gca gtc act gtc tcc tc				368
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Ser Val Lys Phe Ser Cys Lys Val Ser Gly Asp Thr Pro Thr Thr Tyr				
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Tyr Val His Phe Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile				
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Gly Arg Ile Asp Pro Glu Asp Thr Ser Thr Lys Tyr Ala Glu Lys Phe				
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Arg Asn Lys Ala Thr Phe Thr Ala Asp Pro Ser Ser Asn Thr Ala Tyr				
65	70	75	80	
Leu Asn Leu Ser Ser Leu Thr Pro Glu Asp Thr Ala Thr Tyr Phe Cys				
85	90	95		
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<222> (1)...(51)

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48

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15

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51

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42

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<213> Rattus norvegicus

<400> 48

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# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07349

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07 K 16/18; A61 K 39/395; C12 N 5/12, 15/12  
US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/388.1, 388.23; 435/326; 536/23.5; 424/130.1, 139.1, 141.1, 142.1, 145.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

West, US Patent full, STN via medline, caplus, embase, biosis. Search terms, interleukin-18 or IL-18, antibodies, monoclonal, humanized, 2C10, 14B7, 13G9

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	REKVIG et al. Molecular analyses of anti-DNA antibodies induced by polymavirus BK in Balb/c mice. Scandinavian Journal of Immunology. 1995, Vol.41, No.6, pages 593-602. See sequence comparison "A".	14
X	BONILLA et al. V kappa gene usage, idiotype expression and antigen binding among clones expressing the VH <sub>X</sub> 24 gene family derived from naive and anti-idiotype immune Balb/c mice. Journal of Immunology. 15 July 1990, Vol.145, No.2, pages 616-622, see sequence comparison "B"	14

Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means		
"P" document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search  
29 JUNE 2000

Date of mailing of the international search report  
**04 AUG 2000**

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
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Facsimile No. (703) 305-3230

Authorized officer

FOZIA HAMUD

Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

International application No. PCT/US00/07349
---

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JONES et al. Expression of TIMP3 mRNA is elevated in retinas affected by simplex retinitis pigmentosa. FEBS Letters. October 1994, VOL.352, No.2, pages 171-174, see sequence comparison "C"	15
X	EP 0528767 A1 (SANDOZ, LTD.) 24 February 1993 (24.02.93), see page 35, also see sequence comparison "D"	14
A, P	EP 0974600 A2 (KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KASAKU KENKYUJO) 26 January 2000 (26.01.2000), see entire document.	1-26
A	WO 99/09063 A1 (VEDA RESEARCH AND DEVELOPMENT CO. LTD.) 25 February 1999 (25.02.99), see entire document.	1-26

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/07349

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07349

A. CLASSIFICATION OF SUBJECT MATTER:  
US CL :

530/388.1, 388.23; 435/326; 536/23.5; 424/130.1, 139.1, 141.1, 142.1, 145.1

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING  
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-4, 7-8, 11-26, drawn to a rat monoclonal antibody (Rat 2C10) specific for human IL-18, a hybridoma cell line producing said antibody a nucleic acid encoding said antibody, a pharmaceutical composition comprising said antibody, a method of treatment using said antibody and a method of diagnosis using said antibody.

Group II, claims 1-3, 5, 7, 9, 11-26, drawn to a rat monoclonal antibody (Murine 13G9) specific for human IL-18, a hybridoma cell line producing said antibody a nucleic acid encoding said antibody, a pharmaceutical composition comprising said antibody, a method of treatment using said antibody and a method of diagnosis using said antibody.

Group III, claims 1-3, 6-7, 10-26, drawn to a rat monoclonal antibody (Rat 14B7) specific for human IL-18, a hybridoma cell line producing said antibody a nucleic acid encoding said antibody, a pharmaceutical composition comprising said antibody, a method of treatment using said antibody and a method of diagnosis using said antibody.

The inventions listed as Groups I-III do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Pursuant to 37 C.F.R § 1.475 (d), the ISA/US considers that where multiple products and processes are claimed, the main invention shall consist of the first invention of the category first mentioned in the claims and the first recited invention of each of the other categories related thereto. Accordingly, the main invention (Group I) comprises the first-recited product, the Rat 2C10 antibody and the nucleic acid molecule encoding it, a method of using it. Further pursuant to 37 C.F.R § 1.475 (d), the ISA/US considers that any feature which the subsequently recited products and methods share with the main invention does not constitute a special technical feature within the meaning of PCT Rule 13.2 and that each of such products and

INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US00/07349

methods accordingly defines a separate invention.

Vtk2cl0

1 0 30  
 1 D I Q M T Q S P A G L S A S L 15  
 GAC ATT CAA ATG ACC CAG TCT CCA GCT TCC CTG TGT GCA TCT CTG  
 CTG TAA GTT TAC TGG CTC AGA GCT CGA AGG GAC AGA CGT AGA CAC

CDRI 50 70 90 30  
 16 G E T V S I E C L A S E D I Y  
 GGA GAA ACT GTC TCC ATC GAA TCT CTG GCA AGT GAG GAC ATA TAC  
 CCT CTT TGA CGG AGG TAG CTT ACA GAC UGT TCA CTC CTC TAT ATA

31 1 10 13 0 45  
 T Y L T W Y Q Q K P G R S P Q  
 ACT TAT TTA ACA TCC TAT CAG CAG AAA CCA GGG AAA TCT CCT CAA  
 TGA ATA AAT TCT ACC ATA UTC GTC TTT GGT CCC TTT AGA GGA GTT

CDRII 150 1 70 60  
 46 I L T Y G A N K L O D C V P S  
 CTC CTG ATC TAT GGT GCA AAT AAG TTG CAA GAT CGG GTC CCA TCA  
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61 19 0 210 75  
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 GCC AAG TCA CGG TCA CCT ACA CGU TGT GTC ATA AGA GAC TTC TAG

2 30 25 0 270 90  
 76 S G I Q P R D B G D Y F C L Q  
 AGC CGC ATA CAA CCT GAA GAT CAA GGG GAT TAT TTC TGT CTA CGC  
 TCG CGG TAT GTT GGA CTT CTA CTT CGU CTA ATA AAG ACA GAT CTC

CDRIII 2 90 31 0 105  
 91 G S R P P L T F G S G T K L E  
 GGT CGC AAC TTT CGG CTC AUG TTC GGT TCT GGG ACC AAG CTG GAG  
 CGA AGG TTC AAA CGG GAG TGC AAG CGA AGA CGC TGC TTC GAC CTC

106 I K R 108  
 ATC AAA CGG  
 TAG TTT CGG

## FIGURE 1

### 1/6

## VH2C10

1 10 30  
 1 E V Q L Q Q S G A E L V R P C 15  
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 CTC CAG GTC GAT GTC GTC AGA CCC CGA CTC CAA CAC TCT GGA CGC

16 50 70 90  
 16 T S V K L E C K V S G E I S T 30  
 ACC TCT GTG AAG TTA TCT TGC AAA CTT TCT GGC GAA ATA ACT ACA  
 TGG AGA CAC TTC ATT AGA AGC TTT CAA AGA CGG CTT TAT TCA TGT

## CDRI

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 CCT ATC ATA AAC CGC AAA CAC TCC GCT TCC CGA CCT GTC CGA GAC

## CDRII

46 150 1 70  
 46 E W I G R I D P R D D S T K V 60  
 GAA TGG ATA GGA AGG ATT GAT CCT GAG CAT GAT AGT ACT ACT AAA TAT  
 CTT ACC TAT CCT TCC TAA CTA GGA CTC CTA CTA TCA TGA TTT ATA

51 19 0 23 0  
 51 A E R F K D K A T L T A Q T S 75  
 GCT GAC AGG TTC AAA GAC AGG GCG AGC CTC ACT CGA CAA ACA TCC  
 CGA CTC TCC AAC TTT CTG TCC CGC TGC GAG TGA CCT GTT TGT AGG

76 2 30 25 0 270  
 76 S N T A Y L N L S S L T S B D 90  
 TCC AAC ACA CGC TAC CTC AAC CTC AGC AGC CTG ACC TCT GAG GAC  
 AGG TTG TGT CGG ATG GAC TTC GAG TCG TCG GAC TGG AGA CTC CTG

91 2 90 31 0  
 91 T A T Y F C T T W R I Y R D S 105  
 ACT GCA ACT TAT TTT TCT ACC ACA TGG CGG ATA TAC CGA CAT AGG  
 TGA CGT TGA ATA AAA ACA TCG TGT ACC GCC TAT ATG CCT CTA TCA

## CDRIII

106 330 3 50  
 106 S G R P F Y V M D A W G Q G A 120  
 TCT GGC CGC CGC TTC TAT GTT ATG GAT GGC TGG GGT CGA CGA CCT  
 AGA CGG CGG CGG AAG ATA CGA TAC CTA CGC ACU CGA GTT CCT CGA

121 37 0 126  
 121 S V T V S S TCA GTC ACT GTC TCC TCA  
 AGT CAG TGA CAG AGG AGT

## FIGURE 2

Vk13g9

### FIGURE 3

316

VII (363)

## **FIGURE 4**

**4/6**

VK14B7

1      D    I    Q    M    T    Q    S    P    A    S    L    S    A    S    L    15  
 GAT ATT CAA ATG ACG CAG TCT CCA CCT TCC CTC TCT GCA TCT CTC  
 CTA TAA GTT TAC TUC GTC AGA GGT CGA AGG GAC AGA CGT AGA GAC

16     G    E    T    V    S    I    E    C    7    C    CDR I    90    30  
 UGA GAA ACT GTC TCC ATC GAA TGT CTA GCA AGT GAG GAC ATA TAC  
 CCT CTT TGA CAG AGG TAG CTT AGA CAT CGT TCA CTC CTC TAT ATG

31     S    Y    L    A    W    Y    O    Q    K    P    G    K    S    P    Q    45  
 AGT TAT TTA GCA TGG TAT CAN CAC AAG CUA GGG AAA TCT CCT CAG  
 TCA ATA AAT CGT ACC ATA GTT GTC TTC GGT CCC TTT AGA CCA CTC

46     L    L    I    Y    A    T    K    R    L    Q    D    150    CDR II    1    70  
 CTC CCG ATC TAT GCC ACA AAA AGC TTC CAA GAT GGG GTC CCA TCA  
 GAG GAC TAG ATA CGG TGT TTT TCC AAC GTT CTA CCC CAG GGT AGT

61     R    F    S    G    S    G    S    G    T    Q    Y    S    L    K    I    75  
 CGG TTC AGT GGU AGT GGA TCT GGC ACA CAC TAT TCT CTC AAA ATA  
 CCC AAG TAA CGG TCA CCT AGA CCC TGT CTC ATA AGA GAG TTT TAT

76     S    D    M    Q    P    E    D    E    G    D    Y    F    C    230    250    270    90  
 ACC GAC ATG CAA CCT GAA GAT GAA GGG GAT TAT TGT TGT CTA CAG  
 TCC CTG TAC GTT GGA CTT CTA CTT CCC CTA ATA AAG ACA GAT GTC

91     CDR III    2    90    310  
 N    S    K    F    P    V    T    F    G    S    G    T    K    J    B    105  
 ATT TCC AAG TTT CCG GTC AGC TTC GGT TGT GGG ACC AAG CTC CAG  
 TTA AGG TTC AAA GGC CAG TGC AAG CUA AGA CCC TGG TTC GAC CTC

106    I    K    R    108  
 ATC AAA CGC  
 TAC TTT CCC

**FIGURE 5**  
**5/6**

VIIIB7

	1	S V Q L O O S G A E L V R P G	30	1.5
		GAG GTT CGG CTT CGG CGG TGT CGC CCT GAG CTT GTG AGA CCT CGG CTC CAA CTC CAA CGC CGC AGA CGC CGA CTC GAA CAC TCT GGA CGC		
	16	T S V K F S C K V S C D T P T	70	90
		ACC TCT GTG AAG TTT TCT TCA AAA GTT TCT CGC GAT ACC CCT ACA TGG AGA CAU TTC AAA AGA ACG TTT CAA AGA CGG CTA TGG GGA TCT		30
	31	<b>CDR I</b>	110	130
		T Y Y V II F V R Q N P G D G L		
		ACA TAC TAC GTG CAC TTT GAG ACA CAA AGG CCT GGA CGG GGT CTG TGT ATG ATG CAC GTG AAA CAC TCT GTT TTC GGA CCT CTC CCA GAC		45
	46	150	170	<b>CDR II</b>
		E W T G R I D P E D T S T K Y		
		GAA TGG ATA CGA ACC ATT CAT CCT GAG GAT ACT ACT ACT AAA TAT CTT ACC TAT CCT TCC TAA CTA CGA CGC CTA TGA TCA TCA TTT ATA		60
	61	19 II	210	
		A E K F R N K A T F T A D P S		
		GCT GAG AAG TTC AGA AAT AAG CGG ACA TTC ACT GCA GAT CGA TCC CGA CTC TTC AAG TCT TTA TCC CGG TGT AAG TGA CGT CTA GGT AGG		75
	76	230	250	270
		S N T A Y L N I S S L T P E D		
		TCC AAC ACA GCC TAC CTA AAC CGC ACC AGC CCT GAG GAC AGG TTG TGT CGG ATG GAT TTG GAG TCG TCG GAC TUG GGA CTC CTG		90
	91	290	310	105
		T A T Y F C T I M R Y H S T Y		
		ACT GCA ACC TAT TTT TGT ACC ATA ATG CGG TAC CAT AGT ACC TAT TGA CGT TGG ATA AAA ACA TGG TAT TAC CGG ATG GCA TCA TGG ATA		
	106	<b>CDR III</b>	330	350
		R V Y V N D F W G Q G T A V T		
		AGG GTC TAT GTT ATG GAT TTC TCG CGG CAA GGA ACT GCA GTC ACT TCC CAG ATA CAA TAC AAC ACC CGA GAT CCT TGA CGT CAC TGA		120
	121	V S 122		
		GTC TCC TC CGC ACC AC		

## **FIGURE 6**

**6/6**

## SEQUENCE LISTING

<110> Holmes, Stephen D.  
Ho, Yen Sen  
Taylor, Alexander  
Abdel-Moguid, Sherin S.

<120> Recombinant IL-18 Antagonists Useful in  
Treatment of IL-18 Mediated Disorders

<130> P50897

<140> 60/125,299  
<141> 1999-03-19

<160> 48

<170> FastSEQ for Windows Version 3.0

<210> 1  
<211> 324  
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<213> Rattus norvegicus

<220>  
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<222> (1)...(324)  
<223> Light chain V region

<400> 1

gac att caa atg acc cag tct cca gct tcc ctg lut gca tct ctg gga 48  
Asp Ile Gln Met Thr Glu Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly  
1 5 10 15

gaa act gli: tcc atc gaa kgl ctg gca agt gas gac ata tac act kai. 96  
Glu Thr Val Ser Ile Glu Cys Leu Ala Ser Glu Asp Ile Tyr Thr Tyr  
20 25 30

ile acc tgg tat caa cag aaa tca ggg aaa tat cct caa ttc tgg atc 144  
 Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile  
 35 40 45

tat gat gca aat aag ttg caa gat ggg gtc acc leu cgg ttc aat ggc 192  
 Tyr Gly Ala Asn Lys Ile Gln Asp Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

agt gga tct ggc acc cag Ile Ile ttc agg atc aac ggc ata caa tcc 240  
 Ser Gly Ser Gly Thr Cln Tyr Ser Leu Lys Ile Ser Gly Ile Cln Pro  
 65 70 75 80

gaa gat gaa ggg gat Ile Ile tgc ctc cag aat tcc aag Ile tcc ctc 288  
 Glu Asp Glu Gly Asp Tyr Phe Cys Leu Gln Gly Ser Lys Phe Pro Leu  
 85 90 95

aeg ttc aat tct ggg acc aag cly gng atc aat cgg 324  
 Thr Phe Gly Ser Gly Thr Lys Leu Cln Ile Lys Arg  
 100 105

<210> 2  
<211> 108  
<212> PRT  
<213> Rattus norvegicus

<400> 2  
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly  
1 5 10 15  
Glu Thr Val Ser Ile Gln Cys Leu Ala Ser Glu Asp Ile Tyr Thr Tyr  
20 25 30  
Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile  
35 40 45  
Tyr Gly Ala Asn Lys Leu Cln Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Ser Gly Ile Gln Pro  
65 70 75 80  
Gln Asp Glu Gly Asp Tyr Phe Cys Leu Gln Gly Ser Lys Phe Pro Leu  
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg  
100 105

<210> 3  
<211> 33  
<212> DNA  
<213> Rattus norvegicus

<220>  
<221> CDS  
<222> {1}...{33}  
<223> VK2C10 Light Chain CDR I

<400> 3  
ctg gca agt gag gac ata tac act tat tta aca 33  
Leu Ala Ser Glu Asp Ile Tyr Thr Tyr Leu Thr  
1 5 10

<210> 4  
<211> 11  
<212> PRT  
<213> Rattus norvegicus

<400> 4  
Leu Ala Ser Glu Asp Ile Tyr Thr Tyr Leu Thr  
2 5 10

<210> 5  
<211> 21  
<212> DNA  
<213> Rattus norvegicus

<220>  
<221> CDS  
<222> {1}...{21}  
<223> VK2C10 Light Chain CDR II

<400> 5  
ggc gca aat gag ttg ccc gat 21  
Gly Ala Asn Lys Leu Gln Asp  
1 5

<210> 6  
<211> 7  
<212> PRT  
<213> *Rattus norvegicus*

<400> 6  
Gly Ala Asn Lys Leu Gln Asp  
1 5

<210> 7  
<211> 27  
<212> DNA  
<213> *Rattus norvegicus*

<220>  
<221> CDS  
<222> [1]...[27]  
<223> VK2C10 Light Chain CDR III

<400> 7  
ctc cag ggt tcc aac ttt ccc ctc aac  
Leu Gln Gly Ser Lys Phe Pro Leu Thr  
1 5

27

<210> 8  
<211> 9  
<212> PRT  
<213> *Rattus norvegicus*

<400> 8  
Leu Gln Gly Ser Ilys Phe Pro Leu Thr  
1 5

<210> 9  
<211> 378  
<212> DNA  
<213> *Rattus norvegicus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) ... (378)

&lt;223&gt; Heavy chain V region

&lt;400&gt; 9

ttt gtc cag cta cag cag tcc	ggg gct	gtc	atc	ccc	ggg	ccc	4B
Glu Val Gln Ileu Glu Glu Ser Gly	Ala Glu Leu Val Arg Pro Gly Thr						
1	5	10	15				

tct gtg aag tta val lys	aaa gtt tct	ggc gaa ata	agg aaa	ggg tac	96
Ser Val Tyr Ile Ser Cys Lys Val Ser Gly Glu Ile Ser Thr Gly Tyr					
20	25	30			

tat ttc cac ttt gtg agg cga	agg ctt gca cag ggt	ctg gaa tgg	ata	144
Tyr Phe His Phe Val Arg Arg Pro Gly Gln Gly Leu Glu Trp Ile				
35	40	45		

ggg agg att gat cct gag gal	gal agt act aaa tat	gtt gag agg	ttt	192
Gly Arg Ile Asp Pro Cys Asp Ser Thr Lys Tyr Ala Glu Arg Phe				
50	55	60		

aaa gac agg acg ctc act gca	caa acc ttt acc aca	gcc tac	240
Lys Asp Arg Ala Thr Ileu Thr Ala Glu Thr Ser Ser Asn Thr Ala Tyr			
65	70	75	80

atg aac ctc aac acg acc tct	gag gac aat gca act tat	tct tgt	288
Leu Asn Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys			
85	90	95	

acc aca tgg cgg att taa cga gat	agt lut ggc cgc ecc ttc tat	gtt	336
Thr Thr Trp Arg Ile Tyr Arg Asp Ser Ser Gly Arg Pro Phe Tyr Val			
100	105	110	

atg gat gcc tgg gct cca gga	gtt tca gtc act gtc tcc tca		378
Met Asp Ala Trp Gly Gln Gly Ala Ser Val Thr Val Ser Ser			
115	120	125	

&lt;210&gt; 10

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 10

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Thr
1															15
Ser	Val	Lys	Ieu	Ser	Cys	Lys	Val	Ser	Gly	Glu	Thr	Ser	Thr	Gly	Tyr
		20													30
Tyr	Phe	His	Phe	Val	Arg	Arg	Arg	Pro	Gly	Gln	Gly	Ieu	Glu	Trp	Ile
															35
Gly	Arg	Ile	Asp	Pro	Glu	Asp	Asp	Ser	Thr	Lys	Tyr	Ala	Glu	Arg	Phe
															40
Lys	Asp	Arg	Ala	Thr	Leu	Thr	Ala	Gln	Thr	Ser	Ser	Asn	Thr	Ala	Tyr
65					70										80
Leu	Asn	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
															85
Thr	Thr	Trp	Arg	Ile	Tyr	Arg	Asp	Ser	Ser	Gly	Arg	Pro	Phe	Tyr	Val
				100											105
Met	Asp	Ala	Trp	Gly	Gln	Gly	Ala	Ser	Val	Thr	Val	Ser	Ser		
															110
															115
															120
															125

&lt;210&gt; 11

&lt;211&gt; 15

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(15)

&lt;223&gt; VH2C10 Heavy chain CDR I

&lt;400&gt; 11

gga	tac	tat	ttc	cac											15
Gly	Tyr	Tyr	Phe	His											
2				5											

&lt;210&gt; 12

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 12

Gly Tyr Tyr Phe Ile

1 5

&lt;210&gt; 13

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(51)

&lt;223&gt; VH2C10 Heavy chain CDR II

&lt;400&gt; 13

agg att gag cct gag gag agt aca aaa ttt gtc gag agg ttc aaa  
Arg Ile Asp Pro Glu Asp Asp Ser Thr Lys Tyr Ala Gln Arg Phe Lys

48

1 5 10 15

gac

51

&lt;210&gt; 14

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 14

Arg Ile Asp Pro Glu Asp Asp Ser Thr Lys Tyr Ala Gln Arg Phe Lys

1 5 10 15

&lt;210&gt; 15

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(51)

&lt;223&gt; VH2C10 Heavy chain CDR TTT

&lt;400&gt; 15

tgg cca ata tac cga gat agt tct ggc aya acc ttc tat gtt atg val. 48  
 Trp Arg Ile Tyr Arg Asp Ser Ser Gly Arg Pro Phe Tyr Val Met Asp  
 1 5 10 15

gcc 51

<210> 16  
 <211> 16  
 <212> PRT  
 <213> *Baillium norvegicum*

<400> 16

Trp Arg Ile Tyr Arg Asp Ser Ser Gly Arg Pro Phe Tyr Val Met Asp  
 1 5 10 15

<210> 17  
 <211> 342  
 <212> DNA  
 <213> *Mus musculus*

<220>  
 <221> CDG  
 <222> (1)...(342)  
 <223> Light chain V region

<400> 17

gag gtt gtt atg aul. cca act cct ctc tcc ctg cct gtc ayt att gga 48  
 Asp Val Val Met Thr Glu Thr Pro Leu Ser Leu Pro Val Ser Leu Gly  
 1 5 10 15

gat cca gcc lcc atc tct tgc aya tct ayt cag ayc att gta cac ayt 96  
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser  
 20 25 30

aat gya aac acc tat tta cat tgg tac ctg cay aag cca ggc cag tct 144  
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45

cca aag ctc ctg aly lcc aya gtt lcc aac cga ttt tct ggg gtc cca 192  
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro  
 50 55 60

gac aga ttc agt ggc agt gga lca ggt aca mat ttc aca ctc aag atc	240		
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile			
65	70	75	80
aga aca gta gag gct gag gal ctg gga gtt tat ttc tgc tct aca agt	288		
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser			
85	90	95	
aca cat gtt cct aca tcc tcc aca aca ggg aca aca ctg gaa ata	336		
Thr His Val Pro Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile			
100	105	110	
aas cgg	342		
Lys Arg			

<210> 18  
<211> 114  
<212> PRT  
<213> Mus musculus:

<400> 18

Asp Val Val Met Thr Glu Thr Pro Leu Ser Leu Pro Val Ser Leu Gly			
1	5	10	15
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser			
20	25	30	
Asn Glu Asn Thr Tyr Leu His Trp Tyr Leu Glu Lys Pro Gly Gln Ser			
35	40	45	
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro			
50	55	60	
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile			
65	70	75	80
Ser Arg Val Gln Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser			
85	90	95	
Thr His Val Pro Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile			
100	105	110	
Lys Arg			

<210> 19  
<211> 48

<213> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1) ... (48)  
<223> VK13G9 Light Chain CDR I

<400> 19

aga tct agt cag aqc ctt gta cac agt aat gga aac acc acc lnt tta cat 48  
Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His  
1 5 10 15

<210> 20  
<211> 16  
<212> PRT  
<213> Mus musculus

<400> 20

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His  
1 5 10 15

<210> 21  
<211> 21  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1) ... (21)  
<223> VK13G9 Light chain CDR II

<400> 21

aaa gtt tcc aac aca ttt tct 21  
Lys Val Ser Asn Arg Ile Ser  
1 5

<210> 22  
<211> 7  
<212> PRT

<213> Mus musculus

<400> 22

Lys Val Ser Asn Arg Phe Ser

1 5

<210> 23

<211> 30

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(30)

<223> CK13G9 Light chain CDR III

<400> 23

tct cca agt tca cat gtt cct ccc Lac Ser  
Ser Gln Ser Thr His Val Pro Pro Tyr Thr

1 5 10

30

<210> 24

<211> 10

<212> PRT

<213> Mus musculus

<400> 24

Ser Gln Ser Thr His Val Pro Pro Tyr Thr

1 5 10

<210> 25

<211> 369

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(369)

<223> Heavy chain V region

<400> 25

ccc gtt act ctt aat gaa tct ggc cct ggg aat ttg aat ccc leu aag 48  
 Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln  
 1 5 10 15

acc ctc ayt ctg act tct tct tcc tct ggg l.l. act ctg agc acL lcl. 96  
 Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser  
 20 25 30

ggt atg ggt att gcc tgg gtt cgt cag uat tca ggs aag ggc atg gag 144  
 Gly Met Gly Ile Ala Trp Val Arg Gln Pro Ser Gly Lys Gly Leu Glu  
 35 40 45

tgg ctg gca gac att tgg tgg gal. gat eat aat tat tat eat cca tcc 192  
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Asn Lys Tyr Tyr Asn Pro Ser  
 50 55 60

ctg gag aac cag ctc aca ate tcc aag eat acc tcc aga aac cag gta 240  
 Leu Gln Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val  
 65 70 75 80

ttc ctc aac atc acc aat gtg gac act yaa eat tct gcc act eat tac 288  
 Phe Leu Thr Ile Thr Ser Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr  
 85 90 95

tgt gct cgt eat eat tac gac eat agt aac ctc aly eat atg gac tcc 336  
 Cys Ala Arg His His Tyr Asp Gly Ser Ser Leu Leu Pro Met Asp Tyr  
 100 105 110

tgg ggt cca yya acc tca gtc acc gtc tcc tca 369  
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
 115 120

&lt;210&gt; 26

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 26

Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Lys Pro Ser Gln  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser  
 12/21

20	25	30
Gly Met Gly Ile Ala Trp Val Arg Gln Pro Ser Gly Lys Gly Leu Glu		
35	40	45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Asn Lys Tyr Tyr Asn Pro Ser		
50	55	60
Leu Glu Ser Gln Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val		
65	70	75
Ile Leu Thr Ile Thr Ser Val Asp Thr Ala Asp Ser Ala Thr Tyr Tyr		
85	90	95
Cys Ala Arg His His Tyr Asp Gly Ser Ser Leu Leu Pro Met Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser		
115	120	

<210> 27  
<211> 21  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (11...21)  
<223> VH1309 Heavy chain CDR 1

<400> 27	
act tct ggt atg ggt att gcc	21
Thr Ser Gly Met Gly Ile Ala	
1	5

<210> 28  
<211> 7  
<212> PRT  
<213> Mus musculus

<400> 28	
Thr Ser Gly Met Gly Ile Ala	
1	5

<210> 29  
<211> 48  
<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(48)

<223> VH13G9 Heavy chain CDR II

<400> 29

gac a.t. tgg tgg gat gat cat atg tat tat aat cca tcc ctg gag aac  
Asp Ile Trp Trp Asp Asp Asn Lys Tyr Tyr Arg Pro Ser Leu Glu Ser  
1 5 10 15

48

<210> 30

<211> 16

<212> PRT

<213> Mus musculus

<400> 30

Asp Ile Trp Trp Asp Asp Asn Lys Tyr Tyr Asn Pro Ser Leu Glu Ser  
1 5 10 15

<210> 31

<211> 39

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(39)

<223> VH13G9 Heavy chain CDR III

<400> 31

cat cat tac gac ggt agt agc ctc ctg cct atg gag his his  
His His Tyr Asp Gly Ser Ser Leu Leu Pro Met Asp Tyr  
1 5 10

39

<210> 32

<211> 13

<212> PRT

<213> Mus musculus

&lt;400&gt; 32

Bis His Tyr Asp Gly Ser Ser Leu Leu Pro Met Asp Tyr  
 1                   5                   10

&lt;210&gt; 33

&lt;211&gt; 324

&lt;212&gt; DNA

<213> *Rattus norvegicus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; {1}...[324)

&lt;223&gt; Light chain V region

&lt;400&gt; 33

gat ait cca atg ecg eag tct cca gat leu cty het gca tct ctg gga      48  
 Asp Ile Gln Met Thr Glu Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly  
 1                   5                   10                   15

gaa act glc tcc atc gaa tgt cta gca agt gag gac ata tac agt tat      96  
 Glu Thr Val Ser Ile Glu Cys Leu Ala Ser Glu Asp Ile Tyr Ser Tyr  
 20                   25                   30

tta gca tgg tct cca cag eag cca ggg aaa tct ctc cag ctc ctg atc      144  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro Gln Leu Leu Ile  
 35                   40                   45

tat gcc aca aaa eyg ttg cca gat ggg gtc oca tca eyg Ile agt ggc      192  
 Tyr Ala Thr Lys Arg Leu Gln Asp Gly Val Pro Ser Arg Phe Ser Gly  
 50                   55                   60

agt gga tcc ggc aca cag tat tct ctc aaa ata agc gac atg cca cct      240  
 Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Ser Asp Met Gln Pro  
 65                   70                   75                   80

gaa gat gca ggg gat tat ttc tgt cta cag aat leu aag ttt ccg gtc      288  
 Glu Asp Glu Gly Asp Tyr Phe Cys Leu Gln Asn Ser Lys Phe Pro Val  
 85                   90                   95

acg ttc ggt tct ggg ecc eeg ctc gag atc aca cgg      324  
 Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg  
 100                   105

<210> 34  
<211> 108  
<212> PRT  
<213> Rattus norvegicus

<400> 34

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Ala	Ser	Leu	Gly
1					5					10					15
Clu	Thr	Val	Ser	ile	Glu	Cys	Leu	Ala	Ser	Clx	Asp	Ile	Tyr	Ser	Tyr
				20						25					30
Leu	Ala	Tyr	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Ile
				35			40					45			
Tyr	Ala	Thr	Lys	Arg	Leu	Gln	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
			50			55						60			
Ser	Gly	Ser	Gly	Thr	Cln	Tyr	Ser	Leu	Lys	Ile	Ser	Asp	Met	Gln	Pro
			65			70				75			80		
Glu	Asp	Glu	Gly	Asp	Tyr	Phe	Cys	Leu	Gln	Asn	Ser	Lys	Phe	Pro	Val
			85			90						95			
Thr	Phe	Gly	Ser	Gly	Thr	Lys	Ile	Glu	Ile	Lys	Arg				
			100			105									

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<211> 33  
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<220>  
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<400> 35

ctt	gca	agt	gag	gac	ata	tac	agt	tat	tta	gca					33
Leu	Ala	Ser	Glu	Asp	Ile	Tyr	Ser	Tyr	Ile	Ala					
1				5					10						

<210> 36  
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<400> 36  
Leu Ala Ser Glu Asp Ile Tyr Ser Tyr Leu Ala  
1 5 10

<210> 37  
<211> 21  
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<220>  
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<223> CK14B7 Light chain CDR II

<400> 37  
gcc uca aaa agg ttg caa gat  
Ala Thr Lys Arg Leu Gln Asp 21  
1 5

<210> 38  
<211> 7  
<212> PRT  
<213> *Rattus norvegicus*

<400> 38  
Ala Thr Lys Arg Leu Gln Asp  
1 5

<210> 39  
<211> 27  
<212> DNA  
<213> *Rattus norvegicus*

<220>  
<221> CDS  
<222> (1)...(27)  
<223> VK14B7 Light chain CDR III

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cta cag aat tcc aag ttt cog gtc acg 27

Leu Gln Asn Ser Lys Phe Pro Val Thr

1 5

<210> 40  
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<212> PRT  
<213> Rattus norvegicus

<400> 40

Leu Gln Asn Ser Lys Phe Pro Val Thr

1 5

<210> 41  
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<212> DNA  
<213> Rattus norvegicus

<220>

<221> CDS  
<222> (1) . . . (368)  
<223> Heavy chain V region

<400> 41

gag gtt cag ctt aag cag tct ggg gat gag ctt gtg aca cct ggg aac  
Glu Val Gln Leu Cln Cln Ser Cys Ala Glu Leu Val Arg Pro Gly Thr

1 5 10 15

48

tct gtc aag ttt tct tgc aac gtt tct ggc gat aac cct aca aca tcc  
Ser Val Lys Phe Ser Cys Lys Val Ser Gly Asp Thr Pro Thr Thr Tyr

20 25 30

96

tac gtg cac ttt gtg aca aca agg met ggt aca cag ggt ctg gaa tgg ata  
Tyr Val His Phe Val Arg Gln Arg Pro Gly Gln Gly Ile Glu Trp Ile

35 40 45

144

ggc agg att gat ctc gag gat act agt act aas ttt gct gag aag ttc  
Gly Arg Ile Asp Pro Glu Asp Thr Ser Thr Iys Tyr Ala Glu Lys Phe

50 55 60

192

aga aat aag gct aca ttc act gca gat aca tcc tcc aac aca gca tec

240

Arg Asn Lys Ala Thr Phe Thr Ala Arg Pro Ser Ser Asn Thr Ala Tyr			
65	70	75	80
ctt aac ctc aac aac ctt acc cct gaa gac act gca acc tat ttt tgt			288
Ieu Asn Ieu Ser Ser Leu Thr Pro Glu Asp Thr Ala Thr Tyr Phe Cys			
85	90	95	
acc ata atg agg tac cat agt acc tat agg gtc tat gtt atg gtc ttc			336
Thr Ile Met Arg Tyr His Ser Thr Tyr Arg Val Tyr Val Met Asp Phe			
100	105	110	
agg ggt ccc gga aat gtc gtc act gtc tcc le			368
Trp Gly Gln Gly Thr Ala Val Thr Val Ser			
115	120		
<210> 42			
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<212> PRT			
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<400> 42			
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr			
1	5	10	15
Ser Val Lys Phe Ser Cys Lys Val Ser Gly Asp Thr Pro Thr Thr Tyr			
20	25	30	
Tyr Val His Phe Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile			
35	40	45	
Gly Arg Ile Asp Pro Glu Asp Thr Ser Thr Lys Tyr Ala Glu Lys Phe			
50	55	60	
Arg Asn Lys Ala Thr Phe Thr Ala Asp Pro Ser Ser Asn Thr Ala Tyr			
65	70	75	80
Leu Asn Leu Ser Ser Leu Thr Pro Glu Asp Thr Ala Thr Tyr Phe Cys			
85	90	95	
Thr Ile Met Arg Tyr His Ser Thr Tyr Arg Val Tyr Val Met Asp Phe			
100	105	110	
Trp Gly Gln Gly Thr Ala Val Thr Val Ser			
115	120		

<210> 43

<211> 15

<212> DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; {1}...{15}

&lt;223&gt; VH14B7 Heavy chain CDR I

&lt;400&gt; 43

atc tac tac gtq cac

Thr Tyr Tyr Val His

1

5

15

&lt;210&gt; 44

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 44

Thr Tyr Tyr Val His

1

5

&lt;210&gt; 45

&lt;211&gt; 5.1

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; {1}...{51}

&lt;223&gt; VH14B7 Heavy chain CDR II

&lt;400&gt; 45

agg att gat cct gag gag act aat aat tat gct gag gag ttc aca

Arg Ile Asp Pro Glu Asp Thr Ser Thr Lys Tyr Ala Glu Lys Phe Arg

1

5

10

15

48

aat

51

&lt;210&gt; 46

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 46

Arg Ile Asp Pro Glu Asp Thr Ser Thr Lys Tyr Ala Glu Lys Phe Arg  
1 5 10 15

&lt;210&gt; 47

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; {1}...{42}

&lt;223&gt; VκI4B7 Heavy chain CDR III

&lt;400&gt; 47

Met Arg Tyr His Ser Thr Tyr Arg Val Tyr Val Met Asp Phe 42  
Met Arg Tyr His Ser Thr Tyr Arg Val Tyr Val Met Asp Phe  
1 5 10

&lt;210&gt; 48

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 48

Met Arg Tyr His Ser Thr Tyr Arg Val Tyr Val Met Asp Phe  
1 5 10

